Chicken anaemia virus evades host immune responses in transformed lymphocytes

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Efstathios S. Giotis[1*], Alistair Scott[2,3], Lisa Rothwell[4#A], Tuanjun Hu[4#a], Richard Talbot[5], Daniel Todd[2,3], David W. Burt[6], Elizabeth J. Glass[5] and Pete Kaiser[4#b]

[1]Section of Virology, Faculty of Medicine, Imperial College London, St Mary's Campus, Norfolk Place, London W2 1PG, UK

[2]Agri-Food and Biosciences Institute, Belfast, UK

[3]Queen's University Belfast, Belfast, UK

[4]Institute for Animal Health, Compton, United Kingdom

[5]The Roslin Institute and R(D)SVS, University of Edinburgh, UK

[6]The University of Queensland, St. Lucia, QLD 4072, Australia

[#a] Current address: The Roslin Institute and R(D)SVS, University of Edinburgh, UK

[#b] Deceased

*Corresponding author tel: 07896498097, email: e.giotis@imperial.ac.uk

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Abbreviations: ANOVA: analysis of variance; **Bcl**: B-cell lymphoma; **BIRC5**: Baculoviral (inhibitor of apoptosis domain) repeat containing 5; **BLAST**: Basic local alignment search tool; **CARD**: Caspase recruitment domain family; **CCT4**: Chaperonin Containing T-complex polypeptide subunit 4; **CD:** Cluster of differentiation; **CXXCL**: Chemokine (C-X-X-C motif) ligand; **DEDD**: Death effector domain; **DIDO1**: Death inducer-obliterator 1; **HSP**: Heat shock protein; **ICP**: Infected-cell polypeptide; **IFI6**: Interferon alpha-inducible protein 6; **IFIT5**: Interferon induced protein with tetratricopeptide repeats 5; **IFN**: Interferon; I**KK**: Inhibitor of nuclear factor kappa-B kinase; **IL**: Interleukin; **JAK**: Janus kinase; **kDa**: Kilodaltons; **MAPK**: Mitogen activated protein kinase; **meq**: Marek's *Eco*RI-Q-encoded protein; **MIF**: Macrophage migration inhibitory factor; **Mx1**: Myxovirus (influenza virus) resistance 1; **NF-kB:** Nuclear factor kappa-light chain enhancer of activated B cells; **OASL**: 2'-5'-oligoadenylate synthetase Like; **pp38**: phosphorylated 38 kDa phosphoprotein; **SATB1**: Special AT-rich sequence binding protein 1; **SLA**: Src like adaptor; **STAT**: Signal transduction and activator of transcription; **TGF**: Transforming growth factor; **Th:** Helper T cell; **Treg:** Regulatory T cell; **VP:** Viral protein.

Abstract

Chicken anaemia virus (CAV) is a lymphotropic virus that causes anaemia and immunosuppression in chickens. Previously, we proposed that CAV evades host antiviral responses *in vivo* by disrupting T-cell signaling, but the precise cellular targets and modes of action remain elusive. In this study, we examined gene expression in Marek's disease virus transformed chicken T-cell line (MSB-1) after infection with CAV using both a custom 5K immune focused microarray and quantitative Real-time PCR at 24, 48 and 72

h post infection. The data demonstrate an intricate equilibrium between CAV and the host gene expression, displaying subtle but significant modulation of transcripts involved in the T-cell-, inflammation- and NF-κB-signaling cascades. CAV efficiently blocked the induction of type-I interferons and interferon stimulated genes at 72 h. The cell expression pattern implies that CAV subverts host antiviral responses and that the transformed environment of MSB-1 cells offers an opportunistic advantage for virus growth.

Text

Chicken anaemia virus (CAV) is a small, non-enveloped, DNA virus that contains a single-stranded circular genome of 2.3 kb and causes significant economic losses in the production of young birds worldwide. In older birds CAV causes a subclinical disease that compromises vaccination and aggravates secondary coexisting infections especially with Marek's disease virus [1, 2]. The CAV genome encodes 3 partially overlapping open reading frames that are translated to produce the structural VP1 protein (52 kDa), the putative immunomodulatory VP2 protein (24 kDa) and VP3 (13 kDa), which induces apoptosis in infected cells. VP3 or apoptin also induces tumor selective apoptosis in a range of human cancer cells and is a potential anti-cancer therapeutic agent [3].

CAV targets erythroid and lymphoid progenitor cells in the bone marrow and thymus, respectively, while B-cells appear unaffected by the virus [4, 5]. The mechanisms that the virus employs to trigger apoptosis, to evade host anti-viral processes and to exploit the host cellular resources have not been elucidated. We previously reported that in two-week old chickens at 14 days post infection (p.i.) with CAV, pro-apoptotic genes such as the Bcl-2 family member Bcl2-antagonist/killer 1 (BAK1) are upregulated in thymus cells, consistent with the extensive apoptosis of thymus cells that is observed macroscopically

following viral infection [6]. We also observed a significant virus-induced modulation of the expression of genes involved in TCR-signaling. A virus-induced dysregulation of TCR-signalling may provide a strategic mechanism for virus escape from the host immune system. However, given the complexity of genetic and epigenetic alterations in *in vivo* conditions, which can mask important cell signaling events, an *in vitro* system may be more appropriate to systematically dissect the mechanisms involved in viral pathogenesis. CAV can grow in chick embryos and a limited number of transformed B- and T-lymphoblastoid cell lines [7-10]. The most commonly used cell line is the immortalised Marek's disease virus (MDV)-transformed chicken lymphoblastoid cell line MDCC-MSB-1 (MSB-1), which consists of MDV-virus transformed chicken lymphocytes [including mature helper T-lymphocytes ($CD3^+$, $CD4^+$, $CD8^-$, $TCR2^+$)] derived from a MDV T- cell splenic lymphoma. MDV is another economically important poultry disease and is caused by an avian α-herpesvirus that frequently coexists with CAV in infected chicken flocks [11, 12]. Crowley et al used a 20K-oligo microarray chip (ARK Genomics, Roslin Institute, now Edinburgh Genomics) and showed that CAV infection of MSB-1 cells for 24 and 48 h, induced transcripts involved in inflammation, apoptosis, and antiviral activity [13]. Due to the rudimentary annotation of early chicken genome assemblies (2.1 genome assembly), this earlier study identified many transcripts which lacked annotation [13]. Our study aimed to confirm and extend this study by assessing CAV-induced host gene expression using a more extended timeframe of infection, a lower multiplicity of infection (MOI), and an in-house immune-focused microarray chip. This chip was developed by Edinburgh Genomics (Roslin Institute) and had a better coverage of immune-related genes than the other existing chicken microarray chips [14]. The data of the study was re-annotated with the latest chicken genome assembly (Gallus_gallus-5.0; GCA_000002315.3). Employing an immune-focused array can circumvent problems

typically associated with universal arrays, such as the extensive amounts of biological information produced or elimination of relevant data through multiple-testing correction to significance levels.

MSB-1 cells grow in suspension culture and require subculturing at intervals of around 3 days and are resistant to infection by most other avian viruses except retroviruses [15, 16]. The level of cell-associated infectivity reaches a maximum between 36 and 48 h after infection and coincides with the period when maximal levels of viral antigen can be detected by immunofluorescence [17]. We have found that cell-free infectivity peaks between 72 and 84 h p.i. (data not shown), in agreement with previous studies [17]. We conducted a time-course investigation (at 24, 48 and 72 h p.i.) of the host gene expression profile in CAV-infected MSB-1 cells using both a 5K immune-focused microarray cDNA array [14] and quantitative RT-PCR (qRT-PCR). MSB-1 cells were grown and infected with the Cux-1 CAV strain at an MOI of 1 as previously described [15]. Six replicate samples from Cux-1-infected and mock-infected MSB-1 cells were collected at each time point and total RNA was extracted. Total RNA was isolated, evaluated and divided for microarray analyses and qRT-PCR, using previously described procedures and qRT-PCR primers [6]. Samples were processed and hybridised on the immune-focused cDNA microarray representing 5,026 chicken genes (the study's data have been deposited in ArrayExpress; Accession: E-MEXP-1229). Genes with a false discovery rate (FDR) of more than 5% in either set of data were excluded from further analyses. The cut-off fold gene expression change was set at ≥ ±1.5. Ingenuity Pathway Analysis software (Ingenuity Systems, Redwood City, CA) was used to associate differentially expressed genes with biological pathways and functional gene networks, matrix2png v1.2.1 for data clustering, and R v3.3.3 for multidimensional scaling (MDS) of microarray samples. Analyses of the

differences between transcripts from mock and infected cells found with qRT-PCR were carried out using one-way ANOVA and a Bonferroni multiple comparisons test with $p<0.05$ considered significant. For both microarrays and qRT-PCR assays a reference design was used where each experimental sample was compared against a common reference sample, which was obtained by pooling all samples at each time point. This enabled samples to be directly compared with each other.

Prior to differential gene expression analysis, the data from the microarray probes were used for MDS, which displays sample variability in two-dimensional space (Fig. 1A). MDS analysis demonstrated that samples were differentiated by time point along coordinate 1, while coordinate 2 separated samples by treatment status (i.e. infected versus mock samples). Samples from infected (24 h) and mock-infected cells (24 and 48 h), and infected cells at 48 and 72 h were clustered together in two groups, while the mock-infected cells at 72 h were distinct from the rest of the samples, possibly due to the extended culture duration. Using a stringent set of criteria, we found a total of 385 transcripts with FDR$\leq$ 0.05 that were differentially expressed (DE) in CAV-infected cells compared with mock-infected cells at all time points (Fig. 1B and Supplementary data). The most noticeable changes in host gene expression occurred between 48 and 72 h p.i. (Fig. 1B). More transcripts (156) were downregulated than were upregulated (119) at 72 h p.i. and only 18 transcripts overlapped between 48 and 72 h (Fig. 1C and Supplementary data). Overall there were different expression trends at different time points, implying distinct cascades of host gene response.

DE transcripts were updated in annotation terms and gene IDs using probe sequence information and BLAST analysis. The list of updated gene IDs and the expression data were then processed into Ingenuity pathway software and analysed for known "canonical" pathways and biological functions (full analysis is presented in

Supplementary data). Analysis identified diverse biological process categories at 48 h, with the more abundant categories including cell-to-cell signaling and interaction, tissue development and morphology, immune response and molecular transport, possibly relating to the virus need for the host machinery to replicate itself. The most enriched pathways were involved in T-cell signaling. At 72 h the most abundant biological function categories were cell death, cell growth and proliferation, and immunological disease, while the most affected pathways were purine and pyrimidine metabolism, integrin- and glucocorticoid- receptor signaling, and T-cell signaling.

In the heatmap rendering of T-cell receptor signaling, inflammation and cytokine signaling pathways in mock- and CAV-infected cells (Fig. 2A) a complex gene expression pattern is shown, suggestive of deregulated T-cell, proinflammatory and innate immune responses. Activation of mammalian T-cells involves a complex cascade of multiple signal transduction pathways that is initiated at the membrane T-cell receptors (TCR) and results in the transcription of multiple genes within the nucleus. Infection studies in chicken T-cells are compromised by a lack of understanding of the chicken T-cell activation/signaling circuits and further impaired by the partial understanding of the overall chicken immune system, including the type I IFN response, which is the first line of host defence upon virus infection. Downregulation of genes involved in TCR signalling, such as those for TCRα, TCRδ, CD3δ, and upregulation of the genes for CD80, CD83 and the negative TCR signaling regulator, SLA (Fig. 2A), corroborate the CAV–induced T-cell dysfunction that we described *in vivo* [6] and were not reported by Crowley et al [13].

At 24 h p.i. a fatty acid desaturase (FADS6) was upregulated and protein kinase delta 1 (PRKCD) was downregulated. PRKCD plays a critical role in the control of growth, differentiation, and apoptosis [18]. At 48 and particularly 72 h p.i., the pro-inflammatory cytokine MIF, the MAPK signaling components MAP3K3 and CXXC5, the pro-inflammatory

ligand receptor, IFNγ-R2, STAT3 and NF-κB1 were upregulated, showing late activation of the type II IFN response, the inflammation response and NF-κB signaling cascades (Fig. 2A and 2B). A wide range of viruses have been reported to activate the NF-κB pathway to promote virus replication, as NF-κB regulates numerous target genes involved in the host cell cycle and immune responses [19]. Interpretation of CAV infection data is complicated by the presence of integrated and circular copies of the MDV-1 genome [20]. MDV's *ICP4*, *pp38*, and *meq* genes are involved in the maintenance of transformation of MSB-1 cells [21]. MDV miRNAs in MSB-1 cells target the mRNA of IL-18, a proinflammatory cytokine that stimulates IFN-γ production in T-cells [22]. Furthermore, NF-κB is central in MDV neoplastic transformation and the MDV Meq oncoprotein may augment NF-κB transcription by targeting the IKK complex [23]. The observed induction of the type II IFN response and the NF-κB complex in CAV-infected MSB-1 cells at 72 h (Fig. 2B) cannot be attributed to MDV, as normalised comparison between infected and mock samples should have negated any effect of MDV. However, whether aberrant signaling by MDV-proteins (undetectable by microarrays), can exacerbate the induction of NF-κB in the samples infected with CAV cannot be determined in this study.

To identify inherent gene expression trends in the cells that may conceal or intensify CAV-induced changes, such as an effect of the number of copies of MDV, we also compared the basal gene expression of mock MSB-1 cells across the time course (Fig. 2C and full dataset in Supplementary data). We did not observe DE genes involved in the NF-κB complex, but instead we identified a time-dependent upregulation (especially at 72 h) of proliferation- and apoptosis-related TGF-β1 (consistent with the transformed phenotype of MSB-1 cells) and downregulation of transcripts encoding chaperonin proteins (CCT4, HSPA8, HSP90B1), which ensure correct protein folding and prevent apoptosis [24]. CAV VP3 requires a transformed environment to induce apoptosis [25], and the transformed

phenotype of MSB-1 cells may offer an opportunistic advantage to VP3 and to CAV infection. Induction of pro-apoptotic genes (DEDD, DIDO1, CARD11) at 48 h and anti-apoptotic genes (BIRC5 or inhibitor of apoptosis 5) at 72 h in CAV-infected cells compared to mock-infected (Fig. 2A) confirm that apoptosis is an integral part of the pathogenesis of the virus. Viruses have been reported to either induce or block apoptosis or do both at different stages during infection [26]. There is evidence that apoptosis is a prerequisite for CAV replication and facilitates virus escape from the cell [27, 28]. Nevertheless, it cannot be ruled out that the apoptosis seen is also part of a host defence mechanism to prevent CAV spread by early cell death [26].

Combining IPA functional network analysis with differential gene expression analysis (Supplementary data) helped uncover high-confidence genes, such as SATB1, a pleiotropic genome organizer, which was downregulated at 72 h, and SLA, which inhibits TCR signaling [29] and was upregulated at 72 h p.i.. Both genes were found in our *in vivo* studies to be downregulated by CAV infection and were not found as differentially regulated by Crowley et al [13]. MSB-1 cells are distinct both functionally and phenotypically from lymphocytes *in vivo* and the virus-specific modulation of these genes both *in vivo* and *in vitro* implicates their involvement in a viral mechanism for suppression of host antiviral responses possibly by modulating host TCR-signaling, although this requires experimental confirmation.

Validation of gene expression results by qRT-PCR demonstrated a high level of agreement in the measurement of expression of five randomly selected genes (SLA, TGF-β1, SATB1, IFN-β, STAT3) with both technologies (Pearson's correlation coefficient r=0.987 and p=0.0018, Fig. 2D). For further validation of microarray results and for consistency with our previous *in vivo* study [6] we used qRT-PCR to examine the expression levels of transcripts for the signature pro-inflammatory (IL-1β, IL-2, IL-6, IL18 and CXCLi2

(CAF/interleukin-8)), type I IFN (IFN-α and IFN-β), Th1 (Il-3, IL-12α, IL-12β and IFN-γ), Th2 (IL-4 and IL-13) and Treg (IL-10 and TGF-β4) cytokines. Only transcripts that showed significant differential expression are presented in Fig. 3. The results demonstrated subtle overall changes in the transcription of cytokines. At 24 h p.i. the expression of IFN-α, TGF-β4 and IL-13 was moderately induced, while at 48 h we noticed a small but significant induction of IFN-α, IFN-β, TGF-β4 and IL-3, followed by downregulation of these transcripts at 72 h. At 72 h the expression of only IL-1β was increased, while that of other cytokines was either unchanged (IL-6) or downregulated (IL-4, IL-10, IL-13, IL-18). Induction of IFN-α and IFN-β at 24 and 48 h is consistent with the observations of Crowley et al [13]. However, there is a discrepancy between their study, which reported that IL-2, IFN-γ, IL-12α and IL-12β were DE and our study, which did not detect any regulation in expression of these genes. In chickens, as in mammals, interferons are key modulators of immune response; they are induced following viral infection and initiate a signaling cascade through the Janus kinase signal transducer and activator of transcription (JAK-STAT) pathway, leading to the transcriptional regulation of hundreds of IFN-regulated genes (IRGs), which induce an antiviral state in the cells [30-33]. However, analysis of our microarray results showed that host induction of IFN-α at 24 h and IFN-α and IFN-β at 48 h by CAV was not accompanied by differential expression of canonical chicken IRGs, such as Mx1, IFIT5, IFI6 and OASL at either 48 or 72 h. This together with the downregulation of IFN-α and IFN-β at 72 h suggest that both IFN induction and signaling cascades are efficiently blocked by the virus between 48-72 h. Future studies should aim to identify the mediators that CAV uses to disarm the host type-I IFN response.

In this study, we used both qRT-PCR and an immune-focused microarray to screen host responses over 72 h of CAV infection in MSB-1 cells. While overall there was agreement with the gene expression trends described by Crowley et al [13], there were also many

differences. These are possibly due to the lower MOI used in our study, and the more up-to-date chicken genome annotation (*Gallus gallus* 5.0 assembly) that helped us identify new transcripts that may be involved in the pathogenicity of CAV. Crowley et al reported that CAV infection of MSB-1 cells resulted in an initial wave of inflammatory, anti-apoptotic and anti-viral gene expression changes at 24 h, followed by alterations in genes associated with immunosuppression at 48 h. Instead, our study has showed minimal immune response at 24 h, a moderate antiviral response at 48 h and an increased regulation of NF-κB- and apoptosis- related transcripts at 72 h. Our results should prove helpful in elucidating the pathogenic mechanisms of CAV and for future work on CAV in MSB-1 cells i.e. RNA interference studies targeting CAV viral genes.

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Conflict of interest

We declare no conflicts of interest

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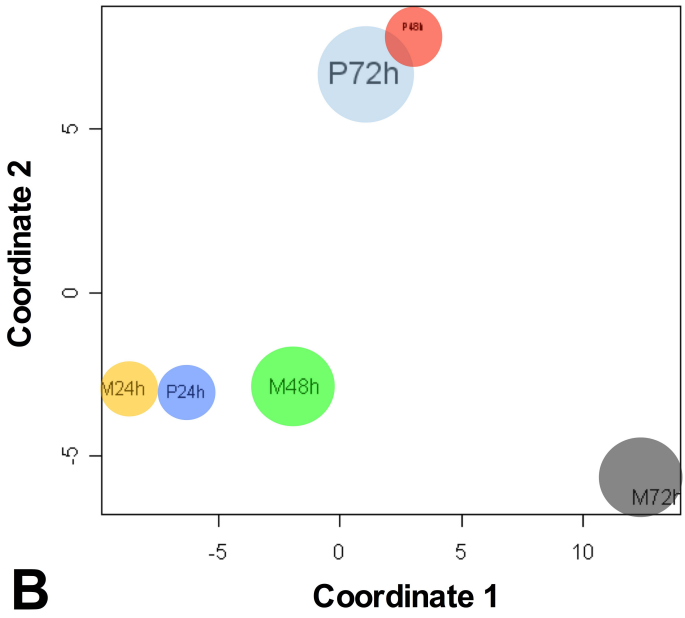
Figure legends

Figure 1: Microarray analysis show distinct immune transcriptional profiles in CAV-infected MSB-1 cells at 48 and 72 h p.i.. (A) Multidimensional scaling plot of microarray data that illustrates the pattern of proximities between the microarray datasets. Each spot represents the replicate samples for mock-infected (Mock -M) and CAV-infected (P) MSB-1 cells at each time point. (B) Number of upregulated and downregulated genes in CAV-infected compared with mock cells at each time point. Only genes showing statistical significance and a fold change ratio ≥ 1.5 were included. (C) Venn diagram of genes showing significant changes (and overlaps) in expression at 24, 48 and 72 h p.i. of MSB-1 cells after infection with CAV.

Figure 2: Microarray analysis shows that CAV-infected MSB-1 cells display a deregulated T-cell, proinflammatory and innate immune response. (A) The heatmap rendering of the indicated signalling pathways in mock- and CAV-infected cells. The ratios are a measure of relative gene expression at each time point compared to reference sample and are depicted according to the color scale shown on the bottom. (B) Ingenuity Pathway Analysis identified NF-κB as the top network signaling pathway at 72 h p.i. in CAV-infected cells. Green represents downregulation while red depicts upregulation while different node shapes represent functional classification. White nodes depict related or neighboring genes. Numbers below nodes denote fold change and significance values. Dotted and solid lines indicate indirect or physical cellular interaction between genes

392 respectively. (C) Comparison of expression levels for 5 selected transcripts determined
393 by microarray and qRT-PCR analysis. (D) Top five upregulated and downregulated genes
394 in mock MSB-1 cells.
395
396 **Figure 3:** qRT-PCR analysis of RNA samples from CAV-infected cells at 24, 48 and 72 h p.i.
397 with a cytokine panel reveals modest transcription changes of immune related genes.
398 Extracted total RNA of CAV-infected and mock-infected MSB-1 cells at each time point was
399 subjected to reverse transcription followed by quantitative PCR using specific primer sets
400 for 10 cytokines normalized against GAPDH (using the ΔΔCt method). Data are
401 representative from three independent experiments. One-way ANOVA with Bonferroni
402 *posthoc* test were used to analyse the data. *, P <0.05, **, P <0.01, ***, P < 0.001, ****, P <
403 0.0001. Broken lines represent fold change=1.
404
405 **Supplementary data** Full list of differentially regulated transcripts between mock-
406 infected and CAV-infected MSB-1 cells at 24, 48, 72 h p.i. and overlapping genes
407 differentially regulated at both 48 and 72 h p.i. and differentially regulated transcripts
408 between mock samples over time. Data enrichment information (Ingenuity pathway
409 analysis) on Ingenuity canonical pathways and biological functions; Analyses include p-
410 value, numbers and names of transcripts implicated in each category.
411

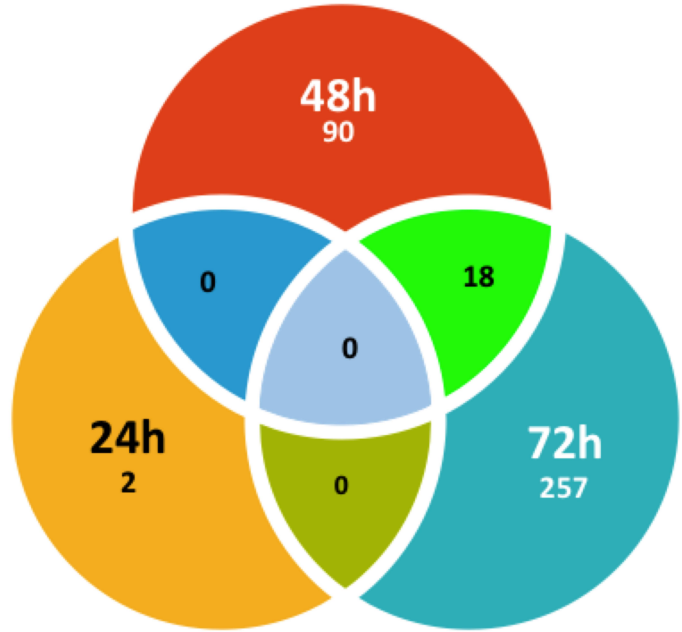
A

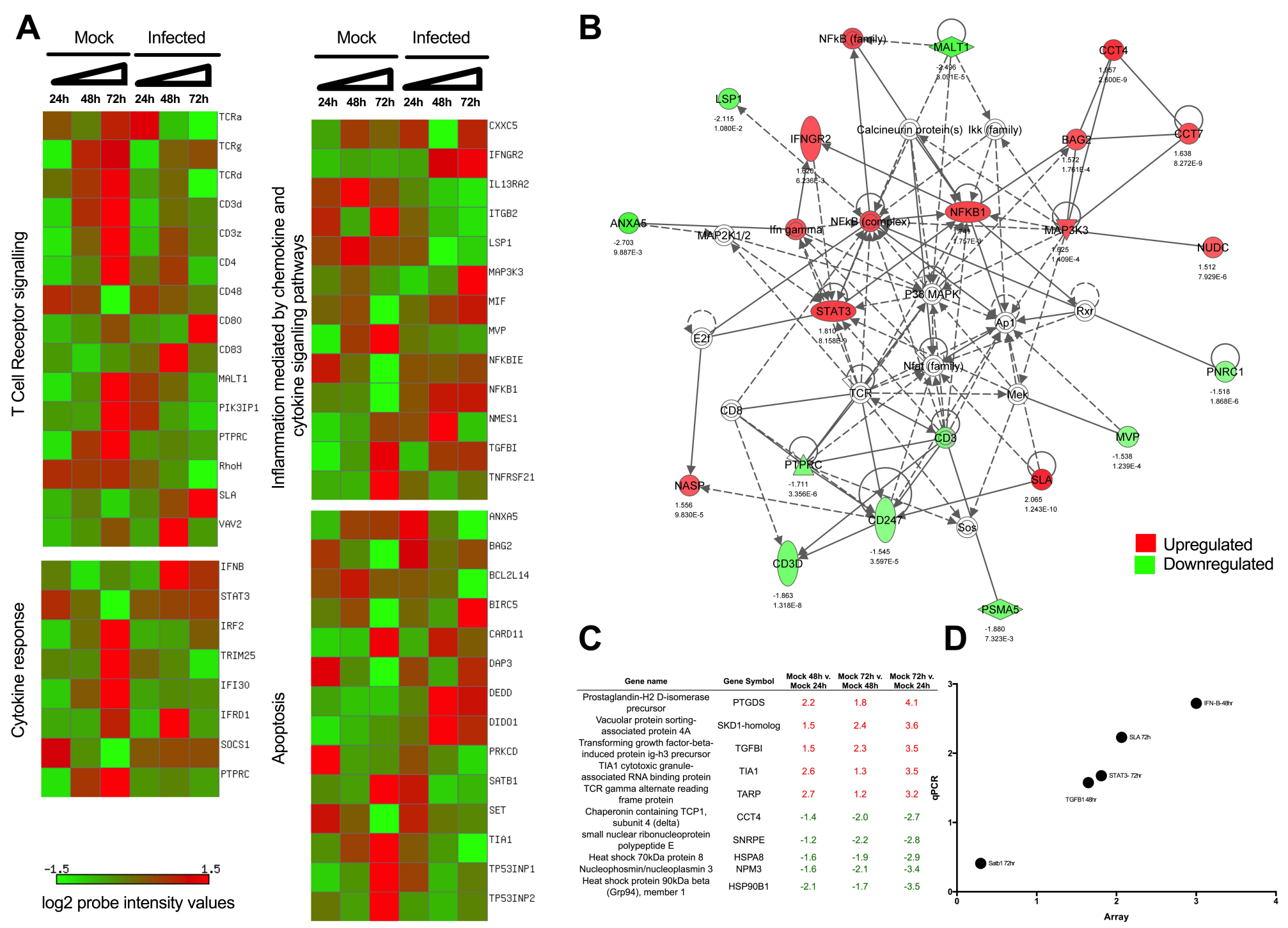


B

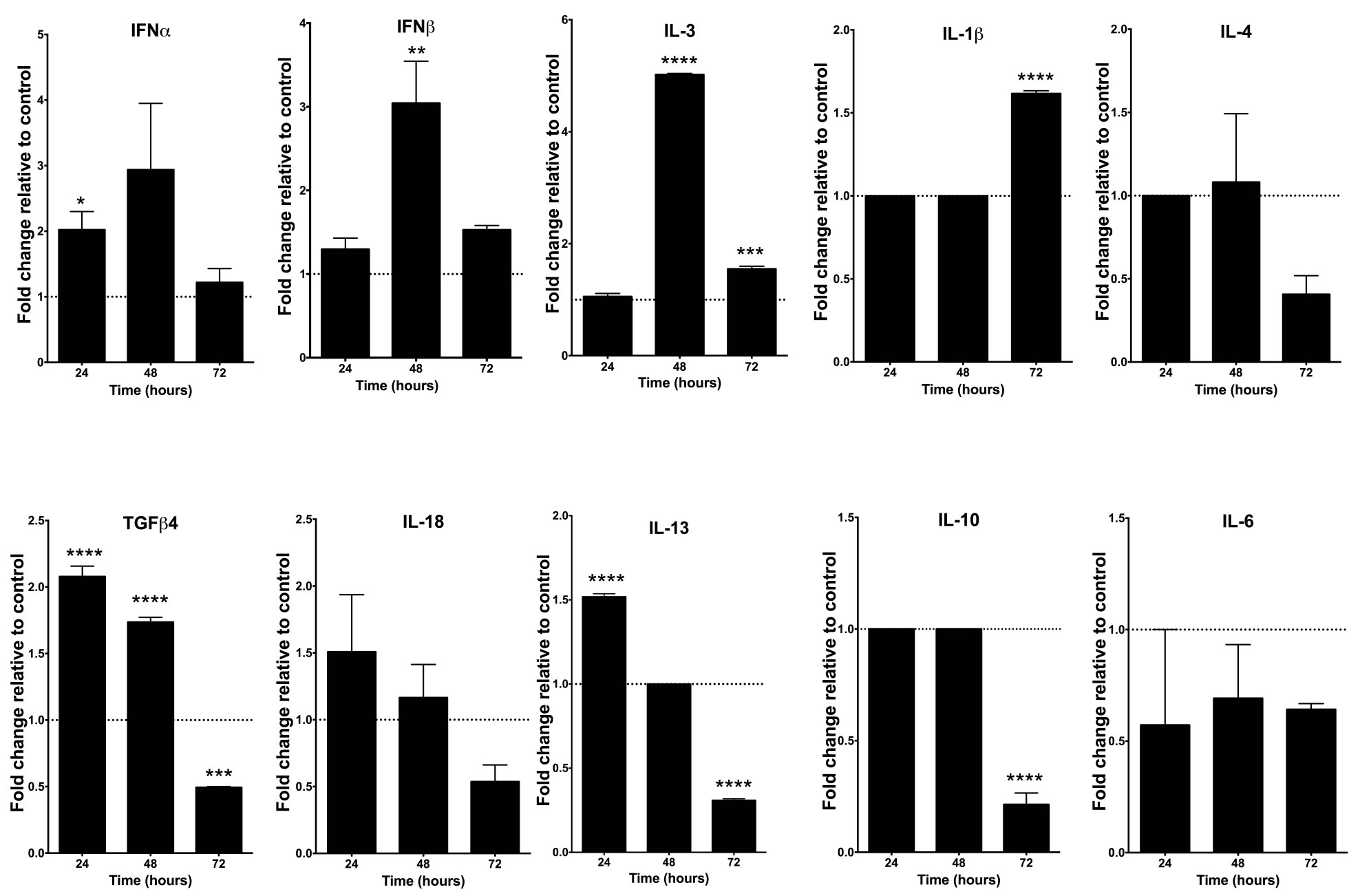
Time (h)	Upregulated	Downregulated	Total
24	1	1	2
48	66	42	108
72	119	156	275

C





Gene name	Gene Symbol	Mock 48h v. Mock 24h	Mock 72h v. Mock 48h	Mock 72h v. Mock 24h
Prostaglandin-H2 D-isomerase precursor	PTGDS	2.2	1.8	4.1
Vacuolar protein sorting-associated protein 4A	SKD1-homolog	1.5	2.4	3.6
Transforming growth factor-beta-induced protein ig-h3 precursor	TGFBI	1.5	2.3	3.5
TIA1 cytotoxic granule-associated RNA binding protein	TIA1	2.6	1.3	3.5
TCR gamma alternate reading frame protein	TARP	2.7	1.2	3.2
Chaperonin containing TCP1, subunit 4 (delta)	CCT4	-1.4	-2.0	-2.7
small nuclear ribonucleoprotein polypeptide E	SNRPE	-1.2	-2.2	-2.8
Heat shock 70kDa protein 8	HSPA8	-1.6	-1.9	-2.9
Nucleophosmin/nucleoplasmin 3	NPM3	-1.6	-2.1	-3.4
Heat shock protein 90kDa beta (Grp94), member 1	HSP90B1	-2.1	-1.7	-3.5


IFNα
IFNβ
IL-3
IL-1β
IL-4
TGFβ4
IL-18
IL-13
IL-10
IL-6
Fold change relative to control
Time (hours)
24
48
72
*
**
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Supplementary data
24 h post infection results

Genbank	Name	Gene symbol	FoldChange	FDRmax	ARKcloneID	P.Value	FDR
AM064974	FADS6 fatty acid desaturase	FADS6	4.59	0.029102231	C0000360p16	1.17E-05	0.031213476
AM065821	Protein kinase-delta1	PRKCD	-1.53	0.044748184	C0000465g23	3.40E-05	0.040049625

48 h post infection results

Genbank	Name	Gene symbol	FoldChange	FDRmax	ARKcloneID	P.Value	FDR
AM064797	5-hydroxymethylcytosine (hmC) binding, ES cell-specific	HMCES	6.91	0.044317654	C0000360h16	0.002369315	0.027033769
AM075291	Von Willebrand factor A domain containing 9	VWA9	6.28	0.017721754	C0000360g14	0.000390191	0.010825392
AM067792	ubiquitin specific peptidase 37	USP37	4.61	0.001633935	C0000476g19	1.01E-05	0.000996701
AM067484	TIA1 cytotoxic granule-associated RNA binding protein (TIA1, TIAL1, TIAR)	TIA1	4.33	0.02974712	C0000474i09	0.00113202	0.018145743
AM065949	SEC31 homolog B (S. cerevisiae)	SEC31B	4.10	0.021354726	C0000465n04	0.000628601	0.013031972
AM065673	polypyrimidine tract binding protein 1	PTBP1	4.09	0.028735258	C0000464p11	0.001081311	0.017582048
AM064852	metastasis suppressor 1-like (MTSS1L), transcript variant X6	MTSS1L	3.84	0.042797934	C0000360k03	0.002218708	0.026248379
AM064983	polymerase (RNA) mitochondrial (DNA directed)	POLRMT	3.83	0.025543189	C0000463a04	0.000819107	0.015581345
AM066174	death inducer-obliterator 1	DIDO1	3.74	0.033417448	C0000467i03	0.001464856	0.020421945
AM064828	PREDICTED: protein lin-37 homolog	LIN37	3.39	0.02529927	C0000360i23	0.000805161	0.015493307
AM067986	porcupine	PORCN	3.09	0.023730441	C0000476p07	0.000731483	0.014475569
BU457418	CD83 molecule	CD83	2.97	0.002035482	603771889F1	1.30E-05	0.001241644
AM070738	heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	2.73	0.004247716	C0000798d19	4.22E-05	0.002591107
X92479	interferon, beta 1, fibroblast (IFN-beta, IFNB)	IFNB	2.72	0.030184133	IFNB gene	0.001172082	0.018412321
AM067700	B6.3 protein	Bu-1	2.71	0.018827453	C0000476c12	0.000460652	0.011526558
AM063225	enoyl-CoA delta isomerase 2	ECI2	2.51	0.003067068	BET603945314K03	2.40E-05	0.001870911
AM069326	trafficking protein, kinesin binding 1	TRAK1	2.37	0.003502086	C0000874m05	3.10E-05	0.002157519

AM071914	collagen, type XXV, alpha 1	COL25A1	2.27	0.042453694	CHK02000039d17	0.002173914	0.025896753
AM071038	acid phosphatase 5, tartrate resistant	ACP5	2.21	0.012065546	C0000853c10	0.000219769	0.007359983
AM071288	PREDICTED: normal mucosa of esophagus-specific gene 1 protein-like isoform 1	NMES1	2.11	0.008012217	C0000853o16	0.000105972	0.004898945
AM063112	No Blast file found		2.09	0.026415653	BET603945381A21	0.000888277	0.01615677
AM075288	golgi glycoprotein 1 (GLG1, CFR)	GLG1	1.93	0.04923001	C0000360a11	0.00291675	0.030030306
AM069011	No Blast file found		1.91	0.000494955	C0000873n11	1.39E-06	0.000321805
AM065277	PHD finger protein 13-like, transcript variant X2	LOC101747338	1.89	0.010591731	C0000463n13	0.000175964	0.006561734
AM069035	protein FAM60A	FAM60A	1.87	0.001133175	C0000873o12	4.31E-06	0.000691237
AM069842	chromosome 4 open reading frame, human CXorf57	C4HXORF57	1.86	0.018436136	C0000878f08	0.000417156	0.011246043
AM069697	leucine-rich repeats and immunoglobulin-like domains 2	LRIG2	1.84	0.006626712	C0000877n19	7.30E-05	0.004072486
AM064561	MOB family member 4, phocein (MOB4, MOBKL3, PHOCN, PREI3)	MOB4	1.82	0.001260427	C0000919L08	6.44E-06	0.000812213
AM063713	nuclear casein kinase and cyclin-dependent kinase substrate 1 (NUCKS1, JC7, NUCKS)	NUCKS1	1.82	0.036456912	JYM603946094K24	0.001656469	0.022238716
AM075540	No Blast file found		1.81	0.001620416	C0000856b07	9.73E-06	0.0009887
AM065904	PREDICTED: serine/threonine-protein kinase MARK2 isoform 2	MARK2	1.76	0.008199583	C0000465k20	0.000114886	0.005042978
AM068208	coatomer protein complex, subunit gamma 2	COPG2	1.76	0.039041986	C0000485j07	0.001852072	0.023815612

AM063131	calcium binding protein 2	CABP2	1.74	0.031583906	BET603945406 K02	0.00127069	0.019266182
AM067852	TP-binding cassette, sub-family C (CFTR/MRP), member 2	ABCC2	1.74	0.01463354	C0000476j10	0.000292905	0.008926459
AM063356	selenoprotein T	SELT	1.73	0.043330461	HFU603551469 I18	0.002261985	0.026431582
AM066489	myosin, light chain 9, regulatory (MYL9, MLC2, myosin, regulatory)	MYL9	1.73	0.044317654	C0000468h10	0.002381001	0.027043553
AM069328	caspase recruitment domain family, member 11	CARD11	1.73	0.000494955	C0000874m07	1.34E-06	0.000315186
AM067851	No Blast file found		1.72	0.010591731	C0000476j11	0.000174637	0.006490443
AM068258	PIGF	PIGF	1.72	0.002953584	C0000485l10	2.11E-05	0.00183595
AM063081	flotillin 2 (FLOT2, flotillin-2)	FLOT2	1.72	0.031631781	BET603945345 I11	0.001285279	0.019300179
AM068541	B-cell translocation gene 1, anti-proliferative	BTG1	1.71	0.044628196	C0000869i03	0.002456516	0.02736906
AM065873	MHC class II antigen	MHC II	1.71	0.000297865	C0000465j08	5.40E-07	0.000181697
AM070074	heat shock 70kDa protein 2 (HSPA2, HSP70)	HSPA2	1.69	0.000165127	C0000892a19	1.32E-07	0.000109484
AM071923	zinc finger protein 207	ZNF207	1.67	0.021166543	CHK02000039e 02	0.000614321	0.012978497
AM067693	death effector domain containing	DEDD	1.67	0.003918438	C0000476c05	3.69E-05	0.002390247
AM067808	transforming growth factor, beta-induced, 68kDa	TGFBI	1.65	0.000796207	C0000476h11	2.71E-06	0.000485686
AM070256	jagunal homolog 1, transcript variant X	JAGN1	1.64	0.002953584	C0000892i22	2.08E-05	0.001801687
AM064395	LOC101750014	LOC101750014	1.64	0.019705179	C0000858l22	0.000499899	0.01202399
AM068360	member RAS oncogene family, transcript variant X2	RAB23	1.64	0.042136566	C0000485p23	0.002135385	0.025703306
AM069461	G protein-coupled receptor kinase 7	GRK7	1.62	0.011856895	C0000877c23	0.000212544	0.007232706
AM067412	No Blast file found		1.62	0.000199896	C0000474e14	2.40E-07	0.00013566

AM068223	LETM1 domain-containing protein 1-like	LOC107049895	1.62	0.040007229	C0000485j22	0.001962062	0.02440441
AM067846	Glyceraldehyde 3-phosphate dehydrogenase	GAPDH	1.61	0.000107483	C0000476j06	4.45E-08	6.56E-05
AM068810	ARP2 actin-related protein 2 homolog (yeast)	ACTR2	1.61	0.043558809	C0000873e10	0.002293028	0.026570874
AM065876	calponin 2	CNN2	1.60	0.000107483	C0000465j11	6.45E-08	0.000100728
AM067844	MpV17 mitochondrial inner membrane protein	MPV17	1.59	0.001260427	C0000476j04	6.56E-06	0.000812607
AM063124	vav 2 guanine nucleotide exchange factor	VAV2	1.58	0.037311302	BET603945395 M23	0.001732631	0.022759894
AM075495	STOM	STOM	1.58	0.031700123	C0000798k16	0.001319781	0.019378168
AM070225	eukaryotic translation initiation factor 1B	EIF1B	1.57	0.006626712	C0000892h13	7.10E-05	0.004042294
AM067677	immunoglobulin gamma heavy chain, S and C regions	HB-15	1.56	0.047511368	C0000476b12	0.002710316	0.028981934
AM070420	LOC101750725	LOC101750725	1.56	0.000107483	C0001665N06	5.76E-08	8.78E-05
AM070627	interferon-related developmental regulator 1 (IFRD1, IFR1)	IFRD1	1.56	0.015046502	C0001705E24	0.000304183	0.009178366
AM071638	LOC417345	LOC417345	1.54	0.003673073	C0000222g08	3.38E-05	0.002246915
AM065870	enhancer of mRNA decapping 3, transcript variant X1	EDC3	1.54	0.01122799	C0000465j04	0.000193207	0.006927181
AM065549	Rho GTPase activating protein 31	ARHGAP31	1.52	0.000297865	C0000464j22	5.96E-07	0.000182778
AM069195	heat shock 70kDa protein 8 (HSPA8, HSC70)	HSPA8	1.50	0.01122799	C0000874f21	0.000191853	0.006849074
AM063898	charged multivesicular body protein 6	CHMP6	-1.51	0.047509004	C0000856a18	0.002700672	0.028980493
BU341330	interleukin 13 receptor, alpha 2	IL13RA2	-1.52	0.031753981	603519773F1	0.001328379	0.01944629
AM065832	Predicted: interleukin 8-like 2	IL8L2	-1.52	0.003502086	CBN1_C00004 65h11.q1kT7S CF	3.15E-05	0.002240574

AM066230	PREDICTED: farnesyl pyrophosphate synthase, partial	FDPS	-1.53	0.030608228	C0000467k21	0.00120453	0.018671019
AM066789	charged multivesicular body protein 2A	CHMP2A	-1.53	0.049087204	C0000653P11	0.002898464	0.029957299
AM065087	deoxyribose-phosphate aldolase (putative)	DERA	-1.54	0.001260427	C0000463f03	6.40E-06	0.000784626
AM063132	tubulin-folding cofactor B	TBCB	-1.54	0.036637034	BET603945407M02	0.001671986	0.022348591
AM065739	solute carrier family 7 (amino acid transporter light chain, L system), member 5	SLC7A5	-1.55	0.000239736	CBN1_C0000465c24.q1kT7SCF	3.84E-07	0.000150526
AM063650	ADP-ribosylarginine hydrolase	ADPRH	-1.56	0.006697365	UEB603581018C06	8.04E-05	0.004143831
AM066680	mitochondrial ribosome recycling factor	MRRF	-1.57	0.000833736	C0000641A17	3.00E-06	0.000508579
AM065826	heme binding protein 2	HEBP2	-1.58	0.000493909	C0000465h05	1.09E-06	0.000301285
AM072025	YTH domain containing 1	YTHDC1	-1.58	0.019705179	CHK02000039i20	0.000517064	0.01205561
AM065992	zinc finger and BTB domain containing 46, transcript variant X8	ZBTB46	-1.58	0.016501636	C0000465p04	0.000347292	0.010065998
AM066494	CXXC5	CXXC5	-1.60	0.026415653	C0000468h15	0.000885358	0.016113548
AM070525	SH3 and PX domains 2A	SH3PXD2A	-1.62	0.031639637	C0001683B19	0.00130351	0.019337075
AM064451	ring finger and CHY zinc finger	RCHY1	-1.63	0.01122799	C0000858o17	0.000193276	0.006944093
AM067339	aminolevulinate, delta-, synthase 1 (ALAS1, ALASN)	ALAS1	-1.66	0.000179482	C0000474b09	1.80E-07	0.000121936
AM065819	ATPase, class VI, type 11C	ATP11C	-1.67	0.012583752	C0000465g21	0.000241801	0.007743647
AM072006	signal sequence receptor, beta (translocon-associated protein beta)	SSR2	-1.69	0.003502086	CHK02000039h22	3.11E-05	0.002199315
AM066233	PREDICTED: tousled-like kinase 2 isoform 2	TLK2	-1.70	0.008012217	C0000467k24	0.000109053	0.004954872
AM066657	Meis homeobox 1	MEIS1	-1.70	0.038469591	C0000468o24	0.001817218	0.02346645

AM063478	apolipoprotein A-I	APOA1	-1.72	0.003454326	UEB603581013I04	2.83E-05	0.002107139
AM066880	PREDICTED: ras-related GTP binding protein D	RRAGD	-1.74	0.004247716	UEB603580980O19	4.25E-05	0.002621548
AM065852	tropomodulin 1	TMOD1	-1.75	0.043330461	C0000465i09	0.002263661	0.026513601
AM064249	UBA domain containing 1, transcript variant X2	UBAC1	-1.76	0.040007229	C0000858e15	0.001977939	0.024468877
AM064389	chromosome 3 open reading frame, human C20orf196	C3H20orf196	-1.77	0.003034972	C0000858l15	2.25E-05	0.001861649
AM069042	high mobility group protein HMGI-C-like	HMGI-C	-1.78	0.007433773	C0000873o19	9.23E-05	0.004534601
AM068392	uncharacterized LOC107052719, transcript variant X1	LOC107052719	-1.81	0.042797934	C0000869b12	0.002213519	0.02610674
AM065003	microfibrillar-associated protein 1 (MFAP1, AMF)	MFAP1	-1.83	0.021166543	C0000463b07	0.000607322	0.012911591
AM071877	argininosuccinate synthase 1	ASS1	-1.86	0.045160636	CHK02000039b19	0.002503902	0.027642186
AM065828	TRMT1L	TRMT1L	-1.87	0.00074841	C0000465h07	2.40E-06	0.00045653
AM066098	uncharacterized LOC107057081	LOC107057081	-1.89	0.032689338	C0000467e07	0.001402686	0.019940496
AM065719	transmembrane protein 86A	TMEM86A	-1.91	0.009592759	C0000465c03	0.000153607	0.005851583
AM066626	ankyrin repeat and SOCS box containing 6	ASB6	-1.97	0.003067068	C0000468n14	2.46E-05	0.001923865
AM066471	vestigial like 1 (Drosophila)	VGLL1	-1.99	0.0092959	C0000468g14	0.000146993	0.005670499
AM066521	sulfotransferase family cytosolic 2B member 1-like	SULT2B1	-2.10	0.028248038	C0000468i18	0.001004404	0.017257043
AM071100	lymphocyte antigen 6 complex, locus E (LY6E, SCA-2)	LY6E	-2.41	0.043944669	CTN1_C0000853f13.q1kT7SCF	0.002339728	0.026859933
AM066655	ring finger protein 213	RNF213	-2.53	0.004368754	C0000468o22	4.46E-05	0.00266494
AM072018	MHC class II antigen B-F minor heavy chain precursor	BLB2	-2.75	0.006626712	CHK02000039i11	7.22E-05	0.004056602
AM067240	collagen, type I, alpha 1	COL1A1	-2.93	0.009079089	C0000473m15	0.000141747	0.005538244

AM067376	coiled-coil domain containing 50	CCDC50	-4.02	0.021166543	C0000474d01	0.000613246	0.012943001
AM070526	lymphocyte-specific protein 1	LSP1	-4.73	0.001133619	C0001683C14	4.99E-06	0.000717583

72 h post infection results

Genbank	Name	Gene symbol	FoldChange	FDRmax	ARKcloneID	P.Value	FDR
AM065441	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (MAFA, L-MAF, MAFL)	L-MAF	2.55	0.02810402	C0000464f04	0.005282	0.01301216
AM067686	stabilin 1	STAB1	2.53	0.02338827	C0000476b22	0.004124	0.01082877
AM071140	small nuclear ribonucleoprotein polypeptide E; SOX13	SNRPE	2.40	1.90E-09	C0000853h10	1.14E-12	8.79E-10
AM068465	nucleophosmin/nucleoplasmin 3	NPM3	2.34	7.86E-07	C0000869e16	4.35E-09	3.64E-07
AM070721	tubulin, alpha 1c	TUBA1C	2.31	5.43E-08	C0000798c21	6.53E-11	2.52E-08
AM064778	ribonucleotide reductase M1	RRM1	2.21	1.35E-07	C0000360g20	3.52E-10	6.26E-08
AM069195	heat shock 70kDa protein 8 (HSPA8, HSC70)	HSPA8	2.19	9.85E-07	C0000874f21	6.31E-09	4.56E-07
AM067522	coiled-coil domain containing 90B	CCDC90B	2.18	0.03408799	C0000474k03	0.006809	0.01578274
AM071776	nicotinamide riboside kinase 2-like	NMRK2	2.16	9.85E-08	C0000222n02	2.17E-10	4.77E-08
AM068181	tubulin alpha-4A chain-like	TUB4A	2.14	2.01E-07	C0000485i01	6.83E-10	9.29E-08
AM064344	proliferating cell nuclear antigen	PCNA	2.11	2.21E-08	C0000858j11	2.22E-11	1.03E-08
AM065483	serum response factor (c-fos serum response element-binding transcription factor)	SRF	2.10	5.82E-05	C0000464g24	1.53E-06	2.70E-05
AM065980	thimet oligopeptidase-like	TOP	2.09	8.22E-07	C0000465o16	4.77E-09	3.81E-07
AM068994	ribonucleotide reductase M2	RRM2	2.07	1.80E-09	C0000873m16	7.22E-13	8.35E-10
AM064025	src-like-adapter (SLA, TG)	SLA	2.07	7.27E-08	C0000856i08	1.24E-10	3.36E-08
AM067991	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	EIF2S1	2.05	0.00108892	C0000476p12	6.97E-05	0.00050417
AM065982	solute carrier family28 (sodium-coupled nucleoside transporter), member2	SLC28A2	2.03	0.01205274	C0000465o18	0.001703	0.00558042
AM070961	CD48 molecule	CD48	2.01	7.27E-08	CTN1_C0000798o19.q1kT7SCF	1.26E-10	3.64E-08
AM065940	slit homolog 1 (Drosophila)	SLIT1	1.99	2.33E-05	C0000465m19	4.56E-07	1.08E-05
AM064375	Lysine (K)-specific demethylase 5A	KDM5A	1.99	1.08E-06	C0000858k22	7.55E-09	5.00E-07
AM066456	xeroderma pigmentosum, complementation group A (XPA, XPAC)	XPA	1.98	0.02346307	C0000468f23	0.004147	0.0108634
AM075275	cyclin-dependent kinase 2	CDK2	1.97	0.00019279	CHK0200003 9g09	7.02E-06	8.96E-05
AM066590	zinc finger protein 650	ZNF650	1.96	0.00081181	C0000468l21	4.68E-05	0.00037587
AM066237	haperonin containing TCP1, subunit 4 (delta)	CCT4	1.96	5.41E-07	C0000467l04	2.60E-09	2.56E-07
AM068963	chromodomain helicase DNA binding protein 7	CHD7	1.94	6.01E-06	C0000873l07	7.34E-08	2.78E-06

AM066378	PREDICTED: ras-related protein Rab-44-like	RAB44	1.94	2.67E-06	C0000468c09	2.51E-08	1.24E-06
AM071012	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	POP5	1.93	0.0008324	C0000853b06	4.87E-05	0.0003854
AM070689	glutathione S-transferase omega 1	GSTO1	1.92	0.00035902	C0000798b11	1.59E-05	0.00016623
AM066433	adhesion regulating molecule 1	ARM1	1.89	0.00016498	C0000468e23	5.75E-06	7.64E-05
AM067574	minichromosome maintenance complex component 5	MCM5	1.89	7.47E-05	C0000474m09	2.07E-06	3.46E-05
AM064062	uncharacterized LOC107049794	LOC107049794	1.89	0.00027954	C0000856k01	1.11E-05	0.00012943
AM069815	baculoviral IAP repeat containing 5 (BIRC5, survivin)	BIRC5	1.88	0.00013162	C0000878e01	4.29E-06	6.09E-05
AM064767	family with sequence similarity 96, member A	FAM96A	1.86	5.14E-06	C0000360g07	5.66E-08	2.38E-06
AM064640	phosphatidylinositol glycan anchor biosynthesis, class T	PIGT	1.86	0.0014721	C0000360a13	0.000106	0.00068158
AM065835	structure specific recognition protein 1	CIIDBP	1.84	0.00018102	C0000465h14	6.38E-06	8.38E-05
AM066813	acyl-CoA synthetase family member 2	ACSF2	1.83	0.00022246	GCX603945511E03	8.28E-06	0.000103
AM067040	lanosterol 14-alpha demethylase	CYP51A1	1.83	0.00279517	C0000473d02	0.000242	0.0012971
AM063713	nuclear casein kinase and cyclin-dependent kinase substrate 1 (NUCKS1, JC7, NUCKS)	NUCKS1	1.82	0.01184898	JYM603946094K24	0.001662	0.00549613
AM063729	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	1.81	1.09E-06	ODP603945718C05	8.16E-09	5.12E-07
AM070662	proteasome (prosome, macropain) subunit, alpha type, 3	PSMA3	1.81	9.06E-07	C0000798a04	5.58E-09	4.19E-07
AM064656	protein MANBAL-like	LOC431205	1.80	1.87E-07	C0000360b05	5.63E-10	8.68E-08
AM068185	fatty acyl-CoA hydrolase precursor, medium chain-like	LOC415787	1.80	2.22E-05	C0000485i05	4.26E-07	1.03E-05
AM063593	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	ARAP3	1.80	5.61E-06	UEB603580948O11	6.63E-08	2.60E-06
AM070664	ADAM metallopeptidase with thrombospondin type 1 motif, 7	ADAMTS7	1.79	1.07E-06	C0000798a06	7.07E-09	4.95E-07
AM071781	lectin, galactoside-binding, soluble, 3	LGALS3	1.79	8.18E-05	C0000222n07	2.36E-06	3.79E-05
AM063986	small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB, SNRB', SNRPB')	SNRPB	1.79	1.19E-07	C0000856g03	2.87E-10	5.52E-08
AM063974	ADP-ribosylation factor 4	ARF4	1.79	1.69E-05	C0000856f10	2.91E-07	7.82E-06
AM069279	heat shock 70kDa protein 8 (HSPA8, HSC70)	HSPA8	1.78	0.00029522	C0000874j18	1.19E-05	0.00013669
AM065606	Protein MEF2BNB isoform 1	MEF2BNB	1.77	1.48E-06	C0000464m12	1.21E-08	6.85E-07
AM067164	uracil-DNA glycosylase	UNG	1.76	7.23E-05	C0000473j02	1.98E-06	3.38E-05

AM063229	heat shock 70kDa protein 8 (HSPA8, HSC70)	HSPA8	1.76	3.45E-05	HFU6035513 20G05	7.88E-07	1.60E-05
AM064943	fms-related tyrosine kinase 3	FLT3	1.76	0.0013228	C0000360o06	9.08E-05	0.00061246
AM071746	thymosin beta 15	TMSB15	1.75	0.00365866	C0000222l16	0.000339	0.00169396
AM063920	No Blast file found		1.74	0.00057849	C0000856b24	2.85E-05	0.0002686
AM063779	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1, NF-KB1)	NFKB1	1.74	0.01239664	ODP6039457 78K19	0.001757	0.00573965
AM066478	leucine rich repeat and sterile alpha motif containing 1	LRSAM1	1.74	9.89E-06	C0000468g21	1.48E-07	4.58E-06
AM069568	tubulin, beta 2C	TUBB2C	1.73	7.86E-07	C0000877h22	4.41E-09	3.72E-07
AM066661	chromatin accessibility complex 1	CHRAC1	1.73	0.00041668	C0000468p05	1.91E-05	0.00019292
AM070692	centrosomal protein 85kDa	CEP85	1.73	0.02749861	C0000798b14	0.005071	0.01273186
AM066105	TNF-related apoptosis inducing ligand-like, transcript variant X1	TRAIL-LIKE	1.72	4.48E-05	C0000467e14	1.08E-06	2.08E-05
AM065943	dynein, light chain, Tctex-type 1	DYNLT1	1.71	0.01405168	C0000465m2 2	0.002095	0.00650593
AM063885	cyclin-dependent kinase 1 (CDK1, CDC2)	CDK1	1.71	3.26E-07	C0000856a04	1.30E-09	1.58E-07
AM065320	fasciculation and elongation protein zeta 1 (zygin I)	FEZ1	1.71	7.93E-06	C0000463p14	1.06E-07	3.67E-06
AM066137	high mobility group nucleosome binding domain 5	HMGN5	1.70	1.95E-07	C0000467g04	6.24E-10	9.01E-08
AM070678	peptidylprolyl isomerase H (cyclophilin H)	PPIH	1.70	1.35E-05	C0000798a23	2.26E-07	6.27E-06
AM065999	phosphoglycerate mutase 1 (brain)	PGAM1	1.69	2.91E-05	C0000465p11	6.17E-07	1.35E-05
AM066678	strawberry notch homolog 2 (Drosophila)	SBNO2	1.69	2.01E-05	SBNO2 strawberry notch homolog 2	3.68E-07	9.31E-06
AM064972	signal recognition particle receptor subunit beta-like	SRPRB	1.68	0.00272515	C0000360p13	0.000232	0.00126174
AM065433	smg-8 homolog, nonsense mediated mRNA decay factor (C. elegans)	SMG8	1.67	3.55E-06	C0000464e20	3.62E-08	1.64E-06
AM064662	FK506 binding protein 3, 25kDa	FKBP3	1.67	7.53E-06	C0000360b12	9.94E-08	3.48E-06
AM066530	platelet-derived growth factor receptor, beta polypeptide	PDGFRB	1.67	1.06E-05	C0000468j04	1.63E-07	4.90E-06
AM072052	acetyl-CoA acetyltransferase 2	ACAT2	1.66	5.47E-05	CHK0200003 9j24	1.42E-06	2.53E-05
AM066709	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	PSMD3	1.66	2.91E-05	C0000643O1 5	6.20E-07	1.36E-05
AM065030	thymidine kinase, cytosolic	TK1	1.65	5.55E-06	C0000463c11	6.34E-08	2.57E-06
AM064721	IMP (inosine 5'-monophosphate) dehydrogenase 2	IMPDH2	1.65	9.63E-06	C0000360e07	1.41E-07	4.46E-06

BU438017	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF	1.65	0.00146059	604141521F1	0.000104	0.00067625
AM067325	uncharacterized LOC107051754	LOC107051754	1.64	0.04062212	C0000474a13	0.008611	0.01880804
AM063607	transmembrane protein 60 (TMEM60, C7orf35)	TMEM60	1.64	3.05E-06	BET603945364O15	2.99E-08	1.41E-06
AM066591	PREDICTED: Nipped-B homolog	NIPBL	1.64	0.01364428	C0000468l22	0.00201	0.0063173
AM072144	chaperonin containing TCP1, subunit 7 (eta)	CCT7	1.64	1.09E-06	CHK02000039o02	8.27E-09	5.14E-07
AM066070	small subunit (SSU) processome component homolog (yeast)	UTP20	1.64	0.00372292	C0000467c24	0.000348	0.00172371
AM070729	beta-1,4-N-acetyl-galactosaminyl transferase 3	B4GALNT3	1.63	0.00346155	C0000798d07	0.000312	0.0016027
AM066027	mitochondrial amidoxime reducing component 2	Mar-02	1.63	0.01150941	C0000467a19	0.001599	0.00532886
AM069690	flap structure-specific endonuclease 1	FEN-1	1.63	0.00026742	C0000877n11	1.05E-05	0.00012382
AM065149	mannosidase, alpha, class 1B, member 1	MAN1B1	1.63	0.00030793	C0000463h19	1.28E-05	0.00014282
AM064729	UPF0454 protein C12orf49 homolog precursor	C12orf49	1.63	0.02092164	C0000360e15	0.003551	0.00969279
AM063749	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	CAD	1.63	0.00030642	ODP603945743E11	1.26E-05	0.00014254
AM063980	mitogen-activated protein kinase kinase kinase 3	MAP3K3	1.63	0.00182854	C0000856f18	0.000141	0.00084661
AM065324	BHLHA15; TECPR1 (tectonin beta-propeller repeat containing 1)	TECPR1	1.62	9.06E-07	C0000463p19	5.62E-09	4.30E-07
BU294744	interferon gamma receptor 2 (interferon gamma transducer 1)	IFNGR2	1.62	0.03192204	603606133F1	0.006236	0.0147799
AM065840	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	PLA2G7	1.62	4.12E-07	C0000465h19	1.73E-09	1.91E-07
AM064952	enoyl CoA hydratase 1, peroxisomal	ECH1	1.61	5.42E-06	C0000360o15	6.07E-08	2.51E-06
AM071894	SEC62 homolog (S. cerevisiae) (SEC62, TLOC1)	SEC62	1.61	3.31E-06	CHK02000039c14	3.32E-08	1.53E-06
AM066592	ATPase, H+ transporting, lysosomal V0 subunit a1 (ATP6V0A1, A1)	ATP6V0A1	1.61	2.01E-05	C0000468l23	3.70E-07	9.37E-06
AM064802	adaptor-related protein complex 1, gamma 1 subunit (), transcript variant X2	AP1G1	1.61	0.00013544	C0000360h21	4.47E-06	6.30E-05
AM072086	primary ciliary dyskinesia homolog (mouse)	DPCD	1.60	0.00063746	CHK02000039l12	3.28E-05	0.00029515
AM066004	FtsJ methyltransferase domain containing 2	FTSJD2	1.60	7.07E-05	C0000465p16	1.90E-06	3.27E-05
AM065572	LIM domain kinase 2 (LIMK2,LIMK)	LIMK2	1.60	7.23E-05	C0000464k22	1.98E-06	3.37E-05
AM065886	N(alpha)-acetyltransferase 25, NatB auxiliary subunit (NAA25, C12orf30)	NAA25	1.60	0.0018008	C0000465j24	0.000138	0.00083377
AM065814	NEDD4 binding protein 2-like 1	N4BP2L1	1.59	0.00545842	C0000465g16	0.000583	0.00252725

AM067252	SET nuclear oncogene	SET	1.59	2.16E-05	C0000473n05	4.07E-07	1.00E-05
AM064871	integrator complex subunit 12	INTS12	1.59	4.48E-05	C0000360l01	1.08E-06	2.07E-05
AM065243	No Blast file found		1.59	0.01496141	C0000463l22	0.002282	0.00693597
AM068034	deoxythymidylate kinase (thymidylate kinase)	DTYMK	1.59	7.85E-07	C0000485b10	4.08E-09	3.63E-07
AM063815	centrin, EF-hand protein, 2	CETN2	1.59	0.00013065	ODP603945821l06	4.23E-06	6.05E-05
AM070466	proteasome (prosome, macropain) subunit, alpha type, 2	PSMA2	1.58	1.33E-05	C0001672A20	2.18E-07	6.16E-06
AM069763	microcephalin 1	MCPH1	1.58	0.01715687	C0000878b09	0.002716	0.00794613
AM066313	cystatin C	CST3	1.58	2.42E-07	C0000467o22	8.71E-10	1.12E-07
AM071734	KH domain containing, RNA binding, signal transduction associated 3	KHDRBS3	1.58	0.01198724	C0000222l03	0.001689	0.00555009
AM065085	BCL2-associated athanogene 2	BAG2	1.57	0.00218913	C0000463f01	0.000176	0.00101357
AM071694	small nuclear ribonucleoprotein D3 polypeptide 18kDa	SNRPD3	1.57	7.33E-06	C0000222j10	9.53E-08	3.39E-06
AM066144	golgi to ER traffic protein 4 homolog (S. cerevisiae) (GET4, C7orf20)	GET4	1.57	0.00010313	C0000467g12	3.14E-06	4.78E-05
AM072222	NOP56 ribonucleoprotein homolog (yeast) (NOP56, NOL5A)	NOP56	1.57	0.00043438	3L03	2.04E-05	0.00020148
AM075321	No Blast file found		1.57	2.00E-06	C0000467g16	1.80E-08	9.25E-07
AM071803	zinc finger, matrin type 5	ZMAT5	1.56	0.00701641	C0000222o09	0.000812	0.0032526
AM064370	LYR motif containing 5	LYRM5	1.56	0.00569013	C0000858k16	0.000615	0.00263453
AM070725	tripartite motif containing 25	TRIM25	1.56	0.0045122	C0000798d01	0.000447	0.0020951
AM064149	LOC100859089; GINS complex subunit 1 (Psf1 homolog)	GINS1	1.56	0.01018681	C0000856p11	0.001357	0.00471649
AM067023	progressive external ophthalmoplegia 1	PEO1	1.56	0.00076356	C0000473b21	4.30E-05	0.00035353
AM066474	hydroxyacylglutathione hydrolase-like	HAGHL	1.56	9.10E-06	C0000468g17	1.27E-07	4.24E-06
AM069131	nuclear autoantigenic sperm protein (histone-binding)	NASP	1.56	0.00140724	C0000874c22	9.83E-05	0.00065155
AM067279	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM7	1.55	0.00214943	C0000473o09	0.000172	0.00099519
AM065676	DnaJ (Hsp40) homolog, subfamily C, member 17	DNAJC17	1.55	0.00151468	C0000464p14	0.00011	0.0007013
AM075355	patched domain containing 1	PTCHD1	1.55	0.00303982	C0000476d12	0.000265	0.00140743
AM064189	nucleoporin 214kDa	NUP214	1.55	0.00326288	C0000858b12	0.00029	0.00151071
AM064811	phenylalanyl-tRNA synthetase, alpha subunit (FARSA, FARSLA, PheRS)	FARSA	1.55	0.00349249	C0000360i06	0.000317	0.00161989
AM071846	mu immunoglobulin heavy chain C region	IGHM	1.55	2.85E-06	CHK02000039a10	2.74E-08	1.32E-06

AM070849	TLC domain containing 1	TLCD1	1.55	0.01649364	C0000798j06	0.002582	0.00763655
AM068974	CD48 molecule	CD48	1.54	5.41E-07	C0000873l19	2.55E-09	2.56E-07
AM066305	arginyl-tRNA synthetase (RARS, LOC416169)	RARS	1.54	1.70E-05	C0000467o14	2.97E-07	7.89E-06
AM065074	LOC422497	LOC422497	1.54	0.01334431	C0000463e14	0.00195	0.00617841
AM066441	PREDICTED: complement receptor type 2-like	CR2	1.54	0.00798439	C0000468f07	0.000986	0.00370042
AM066543	phosphotyrosine phosphatase kappa-like	TROJAN	1.53	0.00166149	C0000468j18	0.000122	0.00076927
AM070267	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	HNRPD	1.53	2.50E-06	C0000892j10	2.30E-08	1.16E-06
AM066159	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	DLST	1.53	0.00195253	C0000467h08	0.000153	0.00090402
AM066593	IQ motif containing GTPase activating protein 1	IQGAP1	1.53	0.00238144	C0000468l24	0.000194	0.00110261
AM066381	RAB19, member RAS oncogene family	RAB19	1.53	0.00451888	C0000468c12	0.00045	0.00209691
AM063336	charged multivesicular body protein 3	CHMP3	1.53	8.67E-05	HFU603551448O12	2.55E-06	4.01E-05
AM065525	Ras association (RalGDS/AF-6) domain family member 2	RASSF2	1.53	1.83E-06	C0000464i20	1.57E-08	8.45E-07
AM070342	transmembrane protein 57	TMEM57	1.52	0.00391344	C0000892m14	0.000373	0.00181192
AM069890	polymerase (DNA directed), delta 2, accessory subunit	POLD2	1.52	0.0061223	C0000878h16	0.000681	0.00283463
AM069085	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	EIF2B2	1.52	1.88E-06	C0000874a18	1.66E-08	8.72E-07
AM064835	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NFKBIE	1.52	1.06E-05	C0000360j08	1.65E-07	4.97E-06
AM068831	CD80 molecule	CD80	1.52	0.01187223	C0000873f07	0.001668	0.00549816
AM064727	LOC100859660	LOC100859660	1.52	0.04114974	C0000360e13	0.008772	0.01905233
AM066145	ADP-dependent glucokinase	ADPGK	1.52	2.28E-05	C0000467g13	4.42E-07	1.05E-05
AM070108	brain protein 44-like	BRP44L	1.51	0.00826854	C0000892c07	0.001028	0.00382834
AM072094	heat shock 70kDa protein 8 (HSPA8, HSC70)	HSPA8	1.51	0.00025242	CHK02000039l21	9.74E-06	0.00011687
AM069616	nuclear distribution C homolog (A. nidulans)	NUDC	1.51	0.00021466	C0000877k02	7.93E-06	9.94E-05
AM066914	PREDICTED: BTB/POZ domain-containing protein KCTD3	KCTD3	1.51	0.00264099	GCX603945622K06	0.000223	0.00122284
AM065570	mbt domain containing 1	MBTD1	1.51	9.84E-06	C0000464k20	1.46E-07	4.55E-06
AM066162	ZPLD1	ZPLD1	1.51	0.00566703	C0000467h11	0.00061	0.00262384
AM070730	death associated protein 3	DAP3	1.51	0.00558867	C0000798d08	0.000598	0.00258755
AM069986	member RAS oncogene family (RAN, RANP1)	RAN	1.50	6.06E-06	C0000878m13	7.52E-08	2.81E-06
AM067693	death effector domain containing	DEDD	1.50	0.00516045	C0000476c05	0.000539	0.00238929

AM065891	nudix (nucleoside diphosphate linked moiety X)-type motif 21	NUDT21	1.50	1.15E-06	C0000465k07	8.99E-09	5.33E-07
AM067418	neural proliferation, differentiation and control 1	NPDC1	-1.50	1.11E-05	C0000474f02	1.80E-07	5.14E-06
AM064613	zyxin	ZYX	-1.50	1.06E-05	C0001620N16	1.65E-07	4.94E-06
AM068454	TIA1 cytotoxic granule-associated RNA binding protein (TIA1, TIAL1, TIAR)	TIA1	-1.50	0.04235822	C0000869e05	0.009106	0.01961186
AM067768	ribosomal protein L10a	RPL10A	-1.50	3.87E-05	C0000476f17	9.09E-07	1.79E-05
AM069256	LOC101749469	LOC101749469	-1.50	1.35E-05	C0000874i16	2.28E-07	6.30E-06
AM065004	eukaryotic translation initiation factor 2C, 4	EIF2C4	-1.51	0.00029525	C0000463b08	1.20E-05	0.0001367
AM066525	F-box protein 9	FBXO9	-1.51	0.00115663	C0000468i22	7.64E-05	0.0005369
AM067296	retinoic acid receptor responder (tazarotene induced) 1 (RARRES1, OCX32)	RARRES1	-1.51	0.04295785	C0000473p03	0.009295	0.01988949
AM071638	LOC417345	LOC417345	-1.51	0.00099287	C0000222g08	6.23E-05	0.0004597
AM069542	No blast file found		-1.51	2.91E-05	C0000877g19	6.17E-07	1.35E-05
AM065123	collagen, type V, alpha 1 (COL5A1, cha1V)	COL5A1	-1.52	8.34E-06	C0000463g16	1.13E-07	3.86E-06
AM066724	proline-rich nuclear receptor coactivator 1	PNRC1	-1.52	7.02E-05	C0000645F18	1.87E-06	3.25E-05
AM069080	zinc finger CCCH-type containing 7B	ZC3H7B	-1.52	4.83E-05	C0000874a13	1.21E-06	2.24E-05
AM064339	insulin induced gene 1	INSIG1	-1.52	0.00086741	C0000858j05	5.16E-05	0.00040161
AM066172	anaphase promoting complex subunit 2	ANAPC2	-1.52	1.61E-05	C0000467i01	2.74E-07	7.47E-06
AM065476	EPS8-like 2	EPS8L2	-1.52	0.00229954	C0000464g17	0.000187	0.00106526
AM071717	DEAD (Asp-Glu-Ala-Asp) box helicase 17	DDX17	-1.53	0.00018526	C0000222k10	6.56E-06	8.58E-05
AM068035	sequestosome 1	SQSTM1	-1.53	7.23E-05	C0000485b11	1.98E-06	3.35E-05
AM075339	No blast file found		-1.53	7.29E-06	C0000473l23	9.34E-08	3.38E-06
AM064675	major vault protein	MVP	-1.54	0.0016688	C0000360c03	0.000124	0.00077368
AM067754	K(lysine) acetyltransferase 5	KAT5	-1.54	0.00581287	C0000476f01	0.000632	0.00269554
AM069278	CD247 molecule (CD247, CD3Z)	CD3Z	-1.54	0.00067817	CTst_C00008 74j17.q1kT7S CF	3.60E-05	0.00031399
AM069768	purinergic receptor P2Y, G-protein coupled, 10	P2RY10	-1.55	0.00035455	C0000878b14	1.55E-05	0.00016416
AM067389	Der1-like domain family, member 3	DERL3	-1.55	0.01603639	C0000474d14	0.002494	0.00742485
AM067934	calpain 2, (m/II) large subunit	CAPN2	-1.55	0.01917793	C0000476n02	0.00317	0.00887938
AM066186	Ras association (RalGDS/AF-6) domain family member 2	RASSF2	-1.55	0.02791065	C0000467i17	0.005231	0.01292776
AM065740	hematopoietically expressed homeobox (HHEX, PROBOX)	HHEX	-1.56	0.02071854	C0000465d01	0.003479	0.00959268
AM067846	Glyceraldehyde 3-phosphate dehydrogenase	GAPDH	-1.56	1.10E-05	C0000476j06	1.75E-07	5.08E-06

AM069035	protein FAM60A	FAM60A	-1.56	0.0038406	C0000873o12	0.000364	0.0017782
AM071226	transmembrane protein 35-like	TMEM35	-1.56	0.01025036	C0000853l17	0.001375	0.00474768
AM070235	PREDICTED: microtubule-actin cross-linking factor 1, isoforms 1/2/3/5-like, partial	MACF1	-1.57	7.88E-05	C0000892h24	2.23E-06	3.65E-05
AM069010	spermidine/spermine N1-acetyltransferase 1	SAT1	-1.57	3.74E-06	C0000873n10	3.89E-08	1.73E-06
AM072025	YTH domain containing 1	YTHDC1	-1.58	0.00540719	CHK02000039i20	0.000575	0.00250353
AM065039	melanoma inhibitory activity family, member 3	MIA3	-1.58	0.02203165	C0000463c20	0.003797	0.01020065
AM065752	zinc finger CCCH domain-containing protein 11A	ZC3H11A	-1.58	2.41E-05	C0000465d14	4.84E-07	1.11E-05
AM064118	runt-related transcription factor 1	RUNX1	-1.59	0.0045122	C0000856n11	0.000448	0.00209525
AM071288	PREDICTED: normal mucosa of esophagus-specific gene 1 protein-like isoform 1	NMES1	-1.59	0.0409644	C0000853o16	0.008722	0.0189832
AM072184	post-GPI attachment to proteins factor 2-like	PGAP2	-1.60	0.0224882	CHK02000039p22	0.003912	0.01041204
AM066970	glutamate dehydrogenase 1	GLUD1	-1.60	0.00093935	JYM603946086K22	5.79E-05	0.00043492
AM068467	ChaC, cation transport regulator homolog 1 (E.coli)	CHAC1	-1.60	4.49E-05	C0000869e18	1.10E-06	2.08E-05
AM063372	potassium channel tetramerisation domain containing 20	KCTD20	-1.61	2.88E-05	HFU603551485I22	5.94E-07	1.33E-05
AM065670	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	LSS	-1.63	0.00228721	C0000464p08	0.000185	0.00105898
AM066756	PREDICTED: Uncharacterised protein LOC769674	LOC769674	-1.63	0.00012143	C0000650l10	3.86E-06	5.62E-05
AM065818	oncoprotein induced transcript 3	OIT3	-1.64	0.03834609	C0000465g20	0.008051	0.01775424
AM075540	No blast file found		-1.64	0.00144386	C0000856b07	0.000102	0.00066851
AM065026	SET domain containing (lysine methyltransferase) 8	SETD8	-1.65	0.00440032	C0000463c07	0.000428	0.00203735
AM065878	PREDICTED: tripeptidyl-peptidase 1	TPP1	-1.66	0.00882726	C0000465j13	0.001133	0.00408702
AM069042	high mobility group protein HMGI-C-like	HMGI-C	-1.66	0.00415173	C0000873o19	0.0004	0.00192225
AM067821	WD repeat domain, phosphoinositide interacting 1	WIPI1	-1.66	0.0021321	C0000476i02	0.00017	0.00098716
AM064390	tumor protein p53 inducible nuclear protein 2	TP53INP2	-1.67	7.27E-08	C0000858l16	1.31E-10	4.11E-08
AM067131	ras homolog family member H	RhoH	-1.67	1.10E-05	C0000473h10	1.76E-07	5.11E-06
AM071706	glutamate receptor, ionotropic, AMPA 1	GRIA1	-1.68	1.74E-07	C0000222j22	4.86E-10	8.04E-08
AM067786	tumor protein p53 inducible nuclear protein 1	TP53INP1	-1.68	0.04511224	C0000476g12	0.009978	0.02088697
AM068392	uncharacterized LOC107052719, transcript	LOC107052719	-1.68	0.03160725	C0000869b12	0.006162	0.01463416
AM064686	A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9, HYPERION)	AKAP9	-1.69	0.01675445	C0000360c18	0.002639	0.00775731

AM065075	adenosine kinase	ADK	-1.70	0.02247363	C0000463e15	0.003905	0.01040529
AM066490	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)	ELN	-1.70	0.02371164	C0000468h11	0.004196	0.01097849
AM065639	PREDICTED: chromodomain-helicase-DNA-binding protein 3-like, partial	CHD3	-1.70	0.0126928	C0000464n23	0.001811	0.00588183
AM075534	LOC101751004	LOC101751004	-1.71	1.27E-06	C0000853o06	1.01E-08	5.86E-07
AM066244	tumor necrosis factor receptor superfamily, member 21 (TNFRSF21, DR6)	TNFRSF21	-1.71	0.00842881	CBN1_C0000467l11.q1kT7SCF	0.001049	0.00390254
AM065717	receptor-type tyrosine-protein phosphatase C precursor	PTPRC	-1.71	0.00010818	C0000465c01	3.36E-06	5.02E-05
AM063908	adenosine deaminase	ADA	-1.72	0.00068226	C0000856b08	3.70E-05	0.00031771
AM067189	dishevelled-binding antagonist of beta-catenin 1 , transcript variant X4	DACT1	-1.72	0.01859562	C0000473k05	0.003029	0.00860977
AM064646	TRAF2 and NCK interacting kinase	TNIK	-1.72	0.00169786	C0000360a19	0.000127	0.00078611
AM065516	noggin 2	NOG2	-1.72	0.01364518	C0000464i11	0.002018	0.0063258
AM064649	paramyosin-like	LOC420107	-1.73	0.04201484	C0000360a22	0.009007	0.01945287
AM068079	PRELI domain containing 1	PRELID1	-1.75	1.08E-06	C0000485d12	7.78E-09	5.10E-07
AM071281	No blast file found		-1.75	5.61E-06	C0000853o08	6.74E-08	2.64E-06
AM066422	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) (ITGB2, CD18)	ITGB2	-1.75	0.00967475	CBN1_C0000468e11.q1kT7SCF	0.001266	0.00447941
AM072172	T cell receptor alpha	TCRalpha	-1.76	0.00857831	CBst_CHK02000039p10.q1kT7SCF	0.001082	0.00397176
AM065739	solute carrier family 7 (amino acid transporter light chain, L system), member 5	SLC7A5	-1.76	5.91E-07	CBN1_C0000465c24.q1kT7SCF	2.96E-09	2.74E-07
AM069691	DHHC-type containing 18, transcript variant X3	ZDHHC18	-1.77	0.00115663	C0000877n13	7.64E-05	0.00053689
AM066236	LOC427029 uncharacterised protein	LOC427029	-1.78	0.01536451	C0000467l03	0.002368	0.00711923
AM071587	unc-51-like kinase 2 (C. elegans)	ULK2	-1.80	0.00075913	C0000222d21	4.25E-05	0.00035148
AM064991	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8	-1.80	0.04297192	C0000463a15	0.009313	0.019896
AM066521	sulfotransferase family cytosolic 2B member 1-like	LOC415852	-1.81	0.03244743	C0000468i18	0.006356	0.01503235
AM066053	EGF-like-domain, multiple 7	EGFL7	-1.82	0.02791065	C0000467c04	0.005226	0.01292621
AM066790	Actin, gamma2	ACTG2	-1.82	9.10E-06	C0000653P03	1.26E-07	4.21E-06
AM065230	KIAA1462	KIAA1462	-1.84	0.03614674	C0000463l08	0.007409	0.01673594
AM071676	BCL2-like 14 (apoptosis facilitator)	BCL2L14	-1.84	0.01204928	C0000222h23	0.0017	0.00557882
AM064738	CD3d molecule, delta (CD3-TCR complex)	CD3D	-1.86	1.57E-06	C0000360f01	1.32E-08	7.26E-07

AM065529	phosphatidylinositol glycan anchor biosynthesis, class C	PIGC	-1.87	0.00768685	C0000464i24	0.000932	0.0035645
AM066655	ring finger protein 213	RNF213	-1.88	0.01710267	C0000468o22	0.002701	0.00791854
AM065143	proteasome (prosome, macropain) subunit, alpha type, 5	PSMA5	-1.88	0.03587341	C0000463h13	0.007323	0.01661205
AM067245	OGT	OGT	-1.89	0.00989919	C0000473m20	0.001302	0.00458954
AM071166	GNAS complex locus	GNAS	-1.90	0.00045267	C0000853i14	2.15E-05	0.00020959
AM066552	vacuolar protein sorting 4 homolog A (S. cerevisiae)	VPS4A	-1.94	7.08E-06	C0000468k04	8.93E-08	3.28E-06
AM066657	Meis homeobox 1	MEIS1	-1.94	0.00238733	C0000468o24	0.000196	0.00110691
AM064422	fra-2 gene	FRA-2	-1.95	1.92E-05	C0000858n09	3.46E-07	8.90E-06
AM067515	LOC769729	LOC769729	-1.95	0.02763434	C0000474j19	0.005116	0.0127947
AM065649	sulfotransferase family 1E, estrogen-preferring, member 1	SULT1E1	-1.96	0.03246838	C0000464o10	0.006375	0.01504335
AM071048	UDP-glucose 6-dehydrogenase	UGDH	-1.97	0.00089409	C0000853c24	5.46E-05	0.00041427
AM069817	cathepsin C	CTSC	-1.98	5.41E-07	C0000878e05	2.44E-09	2.51E-07
AM069285	Epidermal growth factor receptor pathway substrate 15-like 1	EPS15L1	-1.99	5.61E-06	C0000874k01	6.72E-08	2.64E-06
AM068919	T cell receptor delta chain	TCRd	-1.99	0.00094994	C0000873j06	5.89E-05	0.00043982
AM066639	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	FUT11	-2.05	0.02997203	C0000468o03	0.005737	0.01387705
AM072142	phosphoinositide-3-kinase interacting protein 1	PIK3IP1	-2.06	0.00845818	CHK0200003 9n24	0.001058	0.00391614
AM068062	syntaxin binding protein 1	STXBP1	-2.10	0.00760767	C0000485c15	0.000914	0.00352235
AM070526	lymphocyte-specific protein 1; LOC771119	LSP1	-2.11	0.04826822	C0001683C14	0.010801	0.02234819
AM067431	interferon, gamma-inducible protein 30	IFI30	-2.14	9.85E-08	C0000474g02	2.06E-10	4.56E-08
BU376898	fms-related tyrosine kinase	FLT3	-2.15	0.01379543	603812446F1	0.002046	0.00638729
AM067301	LOC428714	LOC428714	-2.16	3.26E-07	C0000473p08	1.30E-09	1.51E-07
AM065666	fibronectin 1	FN1	-2.23	0.03565707	C0000464p04	0.007244	0.01650923
AM067298	ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1	-2.25	1.72E-09	C0000473p05	3.43E-13	7.94E-10
AM066648	cysteinyl leukotriene receptor 2	CYSLTR2	-2.38	0.04634595	C0000468o13	0.010316	0.02145817
AM071279	No blast file found		-2.38	8.74E-09	C0000853o05	7.00E-12	4.05E-09
AM066046	aldehyde oxidase 1	AOX1	-2.44	0.02749861	C0000467b21	0.005075	0.01273733
AM064763	tripartite motif containing 47	TRIM47	-2.47	0.02085304	C0000360g03	0.003519	0.00965496
AM067256	complement factor D (adipsin)	CFD	-2.48	0.02561786	C0000473n10	0.00462	0.01186472
AM066667	mucosa associated lymphoid tissue lymphoma translocation gene 1	MALT1	-2.50	0.00061038	C0000468p11	3.09E-05	0.00028261
AM066091	tripartite motif containing 25	TRIM25	-2.61	0.00370029	C0000467d24	0.000345	0.00171323

AM065719	transmembrane protein 86A	TMEM86A	-2.62	2.41E-05	C0000465c03	4.87E-07	1.12E-05
AM075259	cathelicidin-B1-like	CATHB1	-2.69	0.01364428	C0000222i17	0.002012	0.00631772
AM065683	annexin A5	ANXA5	-2.70	0.04482497	C0000464p21	0.009887	0.02075423
AM066227	PREDICTED: Uncharacterised protein KIAA1671-like	KIAA1671	-3.05	0.02136954	C0000467k18	0.003653	0.0098941
AM063343	patatin-like phospholipase domain containing 3	PNPLA3	-3.07	2.63E-05	JYM603946055M14	5.36E-07	1.22E-05
AM064809	smg-1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	SMG1	-3.19	0.01490534	C0000360i04	0.002267	0.00690117
AM067376	coiled-coil domain containing 50	CCDC50	-3.22	0.01853476	C0000474d01	0.003007	0.00858932
AM070038	SATB homeobox 1	SATB1	-3.35	0.00079094	C0000878o24	4.53E-05	0.0003662

Mock comparisons over time

Genbank	Gene name	Mock 48 h Vs 24 h	Mock 72 h Vs 48 h	Mock 72 h Vs Mock 24 h
AM064840	prostaglandin D2 synthase 21kDa (brain) (PTGDS)	2.24	1.83	4.10
AM066552	SKD1-homolog (Vacuolar protein sorting factor 4A)	1.49	2.41	3.59
AM067808	Transforming growth factor, beta-induced, 68kDa	1.50	2.35	3.51
AM067484	TIA1 cytotoxic granule-associated binding proten	2.64	1.33	3.50
AM069981	TCR gamma alternate reading frame	2.73	1.17	3.18
AM069466	LOC100859882	1.38	2.31	3.17
AM066473	Mitochondrial ribosomal protein L38 (MRPL38)	1.44	2.08	2.99
AM066667	mucosa-associated lymphoid tissue lymphoma translocation protein 1	1.35	2.20	2.98
AM065673	Polypyrimidine tract-binding protein 1, isoform a,	2.00	1.42	2.84
AM067821	WD repeat domain, phosphoinositide interacting 1 (WIPI1)	1.33	2.13	2.84
AM064974	fatty acid desaturase 6-like	1.94	1.45	2.80
AM066658	Sarcoglycan, beta (43kDa dystrophin-associated glycoprotein) (SGCB)	1.33	2.09	2.77
AM071717	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (DDX17)	1.49	1.81	2.70
AM065873	Uncharacterised	1.21	2.21	2.68
AM066366	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish)) (MID1IP1)	1.79	1.47	2.63
AM070038	SATB homeobox 1 (SATB1)	0.90	2.93	2.63
AM067431	Interferon, gamma-inducible protein 30 (IFI30)	1.50	1.74	2.62
AM069080	Uncharacterised	1.46	1.77	2.60
AM063650	Uncharacterised	1.33	1.94	2.58
AM064797	DC12 protein	0.70	3.68	2.56
AM064925	GRB2-related adaptor protein (GRAP)	1.81	1.41	2.55
AM070212	6-phosphogluconolactonase	1.52	1.67	2.54
AM071638	Uncharacterised LOC417345 (LOC417345)	1.34	1.86	2.50
AM068467	ChaC, cation transport regulator homolog 1 (E. coli) (CHAC1)	1.37	1.82	2.49
AM071923	Zinc finger protein 207 (ZNF207)	1.38	1.79	2.47
AM064561	MOB family member 4, phocein (MOB4)	1.27	1.94	2.47
AM065870	Uncharacterised	1.14	2.15	2.46
AM067686	Uncharacterised	1.96	1.25	2.46
AM066460	Mitogen-activated protein kinase 14 (MAPK14)	1.15	2.12	2.44
AM067846	Uncharacterised	1.11	2.19	2.43
AM064738	CD3d molecule, delta (CD3-TCR complex) (CD3D)	1.81	1.33	2.41
AM066186	Ras association (RalGDS/AF-6) domain family member 2 (RASSF2)	1.73	1.36	2.35
AM072184	post-GPI attachment to proteins factor 2-like	1.12	2.08	2.33
AM064440	Uncharacterised	1.31	1.77	2.32

AM072025	YTH domain-containing protein 1-like isoform 3	1.65	1.38	2.28
AM066639	Fucosyltransferase 11 (alpha (1,3) fucosyltransferase) (FUT11)	0.87	2.58	2.26
AM075540	Uncharacterised	1.14	1.98	2.25
AM066113	Cathepsin B (CTSB)	1.21	1.85	2.25
AM065752	Zinc finger CCCH-type containing 11A (ZC3H11A)	1.38	1.63	2.25
AM070420	Uncharacterised	1.32	1.70	2.24
AM067296	Retinoic acid receptor responder (tazarotene induced) 1 (RARRES1)	1.31	1.72	2.24
AM063483	CCAAT/enhancer binding protein (C/EBP), gamma (CEBPG)	1.38	1.62	2.23
AM067554	cell division cycle-associated protein 2	1.29	1.72	2.21
AM065197	Polymeric immunoglobulin receptor (PIGR)	1.41	1.57	2.21
AM063666	Peroxisomal biogenesis factor 5 (PEX5)	1.65	1.33	2.20
AM064497	Crystallin, mu (CRYM)	1.41	1.54	2.18
AM065876	Calponin 2 (CNN2)	1.16	1.87	2.16
AM071587	serine/threonine-protein kinase ULK2	1.33	1.62	2.16
AM063681	Uncharacterised	1.64	1.30	2.13
AM068079	PRELI domain containing 1 (PRELID1)	0.98	2.17	2.13
BU271029	Interleukin 18	1.90	1.12	2.13
AM071706	Glutamate receptor, ionotropic, AMPA 1 (GRIA1)	1.41	1.50	2.12
AM064118	Runt-related transcription factor 1 (RUNX1)	1.87	1.13	2.12
AM068845	Proline-rich nuclear receptor coactivator 1 (PNRC1)	1.12	1.89	2.11
AM069918	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (DDX17)	1.19	1.75	2.09
AM067418	Uncharacterised	1.44	1.45	2.08
AM075288	Uncharacterised	1.35	1.54	2.08
AM068831	Uncharacterised	1.23	1.68	2.07
AM068933	Esterase D (ESD)	1.39	1.49	2.07
AM067735	ankyrin repeat domain-containing protein 57	1.26	1.64	2.06
AM067786	Tumor protein p53 inducible nuclear protein 1 (TP53INP1)	1.15	1.78	2.06
AM068416	Uncharacterised LOC100857204 (LOC100857204)	1.39	1.47	2.04
AM071530	Cyclin L1 (CCNL1)	1.14	1.79	2.04
AM065949	SEC31 homolog B (S. cerevisiae) (SEC31B)	1.29	1.58	2.03
AM067298	ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1)	1.43	1.42	2.03
AM066172	anaphase-promoting complex subunit 2	1.20	1.68	2.03
AM064395	LOC100859882 (LOC100859882)	1.13	1.78	2.02

AM063908	Adenosine deaminase (ADA)	1.14	1.77	2.01
AM065717	Protein tyrosine phosphatase, receptor type, C (PTPRC)	1.55	1.30	2.01
AM075291	Uncharacterised	1.18	1.69	1.99
AM071166	Uncharacterised	1.23	1.62	1.99
AM068744	TruB pseudouridine (psi) synthase homolog 2 (E. coli) (TRUB2)	1.12	1.77	1.98
AM065683	Annexin A5 (Annexin V)	1.86	1.06	1.97
AM063054	DENN/MADD domain containing 5B (DENND5B)	1.37	1.42	1.95
AM069676	Eukaryotic translation elongation factor 1 beta 2 (EEF1B2)	1.26	1.54	1.94
AM071526	SID1 transmembrane family member 2	1.37	1.42	1.94
AM067516	Uncharacterised	1.18	1.64	1.94
AM069278	CD247 molecule (CD247)	1.36	1.41	1.92
AM069010	Spermidine/spermine N1-acetyltransferase 1 (SAT1)	1.17	1.64	1.91
AM067340	Prosaposin (PSAP)	1.17	1.63	1.91
AM068965	Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa (EIF2S3)	1.23	1.54	1.91
AM066091	E3 ubiquitin/ISG15 ligase TRIM25	0.97	1.97	1.91
AM069691	Uncharacterised	0.92	2.07	1.90
AM068455	ATPase, Ca++ transporting, ubiquitous (ATP2A3)	1.36	1.40	1.90
AM067739	Uncharacterised	1.20	1.57	1.89
AM071636	Phosphoglycolate phosphatase (PGP)	1.12	1.68	1.89
AM063982	T-cell receptor gamma Vg3-Jg3	1.93	0.97	1.88
AM067870	Uncharacterised	1.21	1.55	1.88
AM070217	Dihydroorotate dehydrogenase (DHODH)	1.25	1.51	1.88
AM067770	Phospholipase A2 receptor 1, 180kDa (PLA2R1)	1.13	1.65	1.87
AM064422	Uncharacterised	0.88	2.12	1.86
AM069481	Coactosin-like 1 (Dictyostelium) (COTL1)	1.40	1.33	1.86
AM070773	Cytohesin 1 interacting protein (CYTIP)	1.78	1.04	1.86
AM064613	Zyxin (ZYX)	1.35	1.36	1.84
AM067245	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT)	0.84	2.19	1.84
AM067768	Ribosomal protein L10a (RPL10A)	1.40	1.31	1.83
AM066046	Aldehyde oxidase 1 (AOX1)	1.14	1.60	1.82

AM068004	Zinc finger protein 593 (ZNF593)	1.16	1.57	1.82
AM064852	Uncharacterised	1.66	1.09	1.81
AM070285	Ras homolog gene family, member A (RHOA)	1.26	1.43	1.81
AM065739	Solute carrier family 7 (amino acid transporter light chain, L system), member 5 (SLC7A5)	1.44	1.26	1.81
AM064361	Zinc finger protein 706 (ZNF706)	1.27	1.43	1.81
AM064828	protein lin-37 homolog	1.84	0.98	1.80
AM069118	Solute carrier family 38, member 2 (SLC38A2)	1.15	1.56	1.79
AM065272	Arylformamidase (AFMID)	1.42	1.26	1.79
AM064675	Major vault protein (MVP)	1.45	1.23	1.78
AM070256	protein jagunal homolog 1	1.10	1.62	1.78
AM065546	Phosphodiesterase 4A, cAMP-specific (PDE4A)	1.42	1.25	1.78
AM072142	phosphoinositide-3-kinase-interacting protein 1	0.98	1.81	1.77
AM070666	Uncharacterised	0.96	1.84	1.77
AM071251	Dual specificity phosphatase 1 (DUSP1)	1.33	1.32	1.75
AM067521	Uncharacterised	1.27	1.38	1.75
AM067602	Uncharacterised	1.11	1.58	1.75
AM067831	Uncharacterised	1.20	1.45	1.73
AM063268	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B (ANP32B)	1.23	1.40	1.73
AM071279	Uncharacterised	0.83	2.08	1.73
AM063331	Eukaryotic translation initiation factor 3, subunit E (EIF3E)	1.19	1.45	1.72
BU240159	Single immunoglobulin and toll-interleukin 1 receptor (TIR) domain (SIGIRR)	1.61	1.07	1.72
AM069542	Uncharacterised	1.17	1.47	1.72
AM066844	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	0.95	1.80	1.71
AM067243	Uncharacterised	1.54	1.11	1.71
AM066724	Proline-rich nuclear receptor coactivator 1 (PNRC1)	1.13	1.52	1.71
AM068035	Sequestosome 1 (SQSTM1)	0.85	2.00	1.70
AM071288	Chromosome 10 open reading frame, human C15orf48 (C10H15orf48)	1.20	1.42	1.70
AM064796	transmembrane protein 100-like	1.17	1.45	1.70
AM067617	keratin, type I cytoskeletal 20	1.14	1.48	1.69
AM071578	ERO1-like protein alpha isoform 3	1.15	1.46	1.69
AM069789	Vinculin (VCL)	1.41	1.19	1.69
AM069817	dipeptidyl peptidase 1	0.77	2.20	1.68
AM070427	Target of myb1-like 2 (chicken) (TOM1L2)	1.38	1.22	1.68

AM069687	TNF receptor-associated factor 5 (TRAF5)	1.29	1.30	1.68
AM068412	Jun proto-oncogene (JUN)	1.34	1.25	1.68
AM069913	Zinc finger protein 706 (ZNF706)	1.27	1.32	1.67
AM066098	Uncharacterised	1.82	0.91	1.67
AM067769	SEC13 homolog (S. cerevisiae) (SEC13)	0.93	1.77	1.66
AM064002	Uncharacterised	1.56	1.07	1.66
AM071022	Jumonji domain containing 1C (JMJD1C)	1.10	1.51	1.66
AM065842	dipeptidyl peptidase 2	1.38	1.19	1.65
AM065842	dipeptidyl peptidase 2	1.42	1.16	1.65
AM071762	Eukaryotic translation initiation factor 3, subunit H (EIF3H)	1.20	1.37	1.65
AM066578	Uncharacterised	1.17	1.40	1.64
AM063372	Potassium channel tetramerisation domain containing 20 (KCTD20)	1.34	1.22	1.64
AM069072	Uncharacterised	1.13	1.44	1.64
AM065826	Uncharacterised	1.51	1.08	1.63
AM065136	Zinc finger, DHHC-type containing 13 (ZDHHC13)	1.40	1.16	1.63
AM068667	CD3d molecule, delta (CD3-TCR complex) (CD3D)	1.46	1.11	1.63
BU438609	Interferon regulatory factor 2 (IRF2)	1.18	1.37	1.63
AM070880	Apolipoprotein A-I (APOA1)	1.70	0.96	1.63
AM063586	Osteoclast stimulating factor 1 (OSTF1)	1.24	1.31	1.63
AM068208	Uncharacterised	1.19	1.36	1.62
AM064390	Uncharacterised	0.91	1.78	1.62
AM066517	Uncharacterised	1.42	1.14	1.62
AM067871	snRNA-activating protein complex subunit 3	1.17	1.38	1.62
AM069707	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase C precursor	1.19	1.36	1.62
AM071559	MHC BF2 class I (BF2)	1.08	1.49	1.61
AM067844	protein Mpv17-like	1.12	1.45	1.61
AM071665	Uncharacterised	1.21	1.33	1.61
AM071122	Myosin IF (MYO1F)	1.26	1.28	1.61
AM068671	Tumor protein, translationally-controlled 1 (TPT1)	1.13	1.43	1.61
AM067792	Uncharacterised	0.82	1.97	1.61
AM075249	Uncharacterised	1.14	1.41	1.61
AM071076	Uncharacterised	1.11	1.44	1.60
AM067412	Uncharacterised	0.98	1.64	1.60
AM068492	Ring finger protein 185 (RNF185)	1.15	1.39	1.60

AM067504	Xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I) (B4GALT7)	1.11	1.44	1.60
AM066720	Histocompatibility (minor) HA-1 (HMHA1)	1.15	1.39	1.59
AM065878	tripeptidyl-peptidase 1	1.48	1.07	1.59
AM066756	Uncharacterised protein LOC769674	1.28	1.25	1.59
AM068040	Uncharacterised	0.83	1.92	1.58
AM063715	SEC22 vesicle trafficking protein homolog A (S. cerevisiae) (SEC22A)	1.20	1.31	1.58
AM066656	Uncharacterised	1.15	1.37	1.58
AM063705	Heterogeneous nuclear ribonucleoprotein D-like (HNRPDL)	1.24	1.27	1.57
AM070371	FK506-binding protein 15	1.08	1.45	1.57
AM069768	Purinergic receptor P2Y, G-protein coupled, 10 (P2RY10)	0.94	1.66	1.56
AM066227	Uncharacterised protein KIAA1671-like	0.95	1.64	1.56
AM070394	Uncharacterised	1.23	1.27	1.56
AM063717	Protein kinase N2 (PKN2)	1.24	1.26	1.56
AM071765	Anti-apoptotic NR13 (NR13)	1.27	1.23	1.56
AM070838	collagen alpha-2(VI) chain precursor	1.12	1.39	1.56
AM067006	cyclin-dependent kinase 12 isoform 2	1.27	1.23	1.56
AM068944	regulator of G-protein signaling 1	1.31	1.19	1.56
AM066174	Death inducer-obliterator 1 (DIDO1)	1.28	1.21	1.55
AM067267	Neuron navigator 3 (NAV3)	1.26	1.22	1.55
AM066704	Eukaryotic translation initiation factor 4B (EIF4B)	1.13	1.36	1.54
AM071319	Uncharacterised	0.98	1.58	1.54
AM075339	Uncharacterised	0.96	1.61	1.54
AM072147	MHC BF2 class I (BF2)	1.19	1.29	1.54
AM067791	Uncharacterised	1.15	1.34	1.54
AM067389	Der1-like domain family, member 3 (DERL3)	1.15	1.34	1.54
AM067389	Der1-like domain family, member 3 (DERL3)	1.21	1.26	1.53
AM067354	Deoxyribonuclease I-like 3 (DNASE1L3)	1.31	1.17	1.53
AM064763	tripartite motif-containing protein 47-like	0.72	2.13	1.53
AM064763	tripartite motif-containing protein 47-like	1.12	1.36	1.53
AM067537	Microtubule-actin crosslinking factor 1 (MACF1)	1.20	1.28	1.53
AM065516	Noggin 2 (NOG2)	0.88	1.73	1.53

AM066706	Enhancer of mRNA decapping 3 homolog (S. cerevisiae) (EDC3)	1.41	1.08	1.52
AM063277	Lysosomal-associated membrane protein 3 (LAMP3)	1.17	1.30	1.52
AM066790	Actin, gamma 2, smooth muscle, enteric (ACTG2)	1.31	1.17	1.52
AM066573	Polymerase (DNA directed), lambda (POLL)	1.40	1.09	1.52
AM071048	UDP-glucose 6-dehydrogenase (UGDH)	1.09	1.39	1.52
AM071914	Collagen, type XXV, alpha 1 (COL25A1)	1.15	1.31	1.51
AM068792	Solute carrier family 2 (facilitated glucose transporter), member 3 (SLC2A3)	1.16	1.30	1.51
AM066509	RAB11B, member RAS oncogene family (RAB11B)	1.45	1.04	1.51
AM067043	microtubule-actin cross-linking factor 1	1.11	1.37	1.51
AM067515	Uncharacterised protein LOC426064	0.86	1.75	1.51
BU114872	Interleukin 16 (lymphocyte chemoattractant factor) (IL16)	1.17	1.30	1.51
AM066525	F-box protein 9 (FBXO9)	1.12	1.35	1.51
AM069311	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (DDX42)	1.16	1.29	1.51
AM066075	Influenza virus NS1A binding protein (IVNS1ABP)	1.50	0.58	0.88
AM065040	SAFB-like, transcription modulator	0.64	1.29	0.83
AM065320	Fasciculation and elongation protein zeta 1 (zygin I) (FEZ1)	1.23	0.60	0.73
AM065907	Archain 1 (ARCN1)	0.72	1.02	0.73
AM071045	Thymidylate synthetase (TYMS)	1.12	0.66	0.73
AM065310	C-type lectin domain family 2 member D-like (LOC776458)	0.90	0.81	0.73
AM067164	Uracil-DNA glycosylase (UNG)	0.97	0.75	0.73
AM071267	bromodomain-containing protein 4	0.92	0.80	0.73
AM065950	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B (ANP32B)	0.91	0.81	0.73
AM071137	methylosome subunit pICln	0.95	0.77	0.73
AM068562	Prohibitin 2 (PHB2)	0.86	0.85	0.73

AM066395	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 (ARHGEF6)	0.70	1.04	0.73
AM069631	Glutaredoxin 5 (GLRX5)	0.83	0.88	0.73
AM069631	Glutaredoxin 5 (GLRX5)	0.89	0.81	0.73
AM064388	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits (GNPTAB)	0.87	0.84	0.73
AM063981	Smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) (SMU1)	0.87	0.84	0.73
AM064952	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial-like	1.16	0.62	0.73
AM068006	Uncharacterised	0.84	0.87	0.73
AM068462	Formin binding protein 4 (FNBP4)	0.78	0.93	0.73
AM072052	Acetyl-CoA acetyltransferase 2 (ACAT2)	1.11	0.65	0.73
AM069527	Uncharacterised protein LOC428145	0.91	0.80	0.72
AM066881	Uncharacterised	0.93	0.78	0.72
AM068153	Uncharacterised	0.86	0.84	0.72
AM070267	Heterogeneous nuclear ribonucleoprotein D-like (HNRPDL)	1.12	0.64	0.72
AM069077	Uncharacterised	0.88	0.82	0.72
AM072006	Signal sequence receptor, beta (translocon-associated protein beta) (SSR2)	0.83	0.87	0.72
AM068821	Selenoprotein W, 1 (SEPW1)	0.93	0.77	0.72
AM065225	ubiquitin-like modifier-activating enzyme 1	0.86	0.84	0.72
AM065319	meprin A subunit beta-like	0.77	0.93	0.72
AM068041	Growth hormone inducible transmembrane protein (GHITM)	0.92	0.78	0.72
AM066140	Jumonji domain containing 1C (JMJD1C)	1.15	0.63	0.72
AM072175	GON-4-like protein	0.65	1.11	0.72
AM069999	Transmembrane protein 18 (TMEM18)	0.82	0.88	0.72
AM070210	Stomatin (EPB72)-like 2 (STOML2)	0.87	0.83	0.72
AM066832	Chromosome 2 open reading frame, human C9orf4 (C2H9orf4)	0.88	0.82	0.72
AM067283	Chromosome 5 open reading frame, human C15orf24 (C5H15orf24)	0.86	0.83	0.72
AM065840	U3 small nucleolar ribonucleoprotein protein IMP3	0.92	0.78	0.72
AM071760	Mitochondrial ribosomal protein S16 (MRPS16)	0.95	0.75	0.71
AM071915	Vacuolar protein sorting 37 homolog B (S. cerevisiae) (VPS37B)	0.92	0.78	0.71
AM063250	transforming growth factor beta-2	0.88	0.81	0.71

AM072107	Eukaryotic translation initiation factor 4A3 (EIF4A3)	0.90	0.79	0.71
AM067376	Coiled-coil domain containing 50 (CCDC50)	1.44	0.49	0.71
AM066000	Ephrin-B1 (EFNB1)	0.91	0.78	0.71
AM063799	Tubulin, gamma 1 (TUBG1)	0.78	0.91	0.71
AM068139	zinc finger and BTB domain-containing protein 26	0.98	0.73	0.71
AM064189	nuclear pore complex protein Nup214	0.96	0.73	0.71
AM067259	Phosphatidic acid phosphatase type 2 domain containing 1B (PPAPDC1B)	0.79	0.89	0.71
AM070813	Sorting nexin 1 (SNX1)	0.86	0.82	0.71
AM069685	THO complex 5 (THOC5)	0.84	0.84	0.71
AM066456	DNA repair protein complementing XP-A cells homolog	1.21	0.58	0.71
AM068149	serine/threonine-protein kinase DCLK3	0.81	0.87	0.71
AM063046	histone H1.10	0.96	0.73	0.70
AM066472	F-box/LRR-repeat protein 5 isoform 1	0.83	0.84	0.70
AM070198	uroporphyrinogen decarboxylase	0.84	0.84	0.70
AM067522	Coiled-coil domain containing 90B (CCDC90B)	0.95	0.74	0.70
AM063600	Family with sequence similarity 136, member A (FAM136A)	0.87	0.80	0.70
AM075364	Uncharacterised	0.88	0.80	0.70
AM067578	Geminin, DNA replication inhibitor (GMNN)	0.93	0.76	0.70
AM071307	thioredoxin-like 4A isoform 2	0.81	0.86	0.70
AM063096	Translin-associated factor X (TSNAX)	0.85	0.82	0.70
AM066590	Uncharacterised	1.25	0.56	0.70
AM063707	Synaptojanin 2 (SYNJ2)	0.74	0.94	0.70
AM068536	Hematological and neurological expressed 1 (HN1)	0.87	0.80	0.70
AM069775	Chromosome 10 open reading frame, human C15orf42 (C10H15orf42)	1.15	0.60	0.70
AM068973	Peroxiredoxin 1 (PRDX1)	0.87	0.80	0.70
AM064068	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (NDUFA12)	0.90	0.77	0.70
AM066004	cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1-like	1.20	0.58	0.70
AM069253	SLIT-ROBO Rho GTPase-activating protein 3-like	0.91	0.76	0.70
AM064721	IMP (inosine 5'-monophosphate) dehydrogenase 2 (IMPDH2)	1.10	0.63	0.69

AM068034	Deoxythymidylate kinase (thymidylate kinase) (DTYMK)	1.11	0.63	0.69
AM070664	Uncharacterised	1.08	0.64	0.69
AM069760	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1)	0.97	0.71	0.69
AM066856	Uncharacterised	0.89	0.78	0.69
AM064054	Uncharacterised	0.86	0.81	0.69
AM063626	THO complex 4 (THOC4)	0.88	0.79	0.69
AM068111	Uncharacterised	0.91	0.76	0.69
AM070569	NAD synthetase 1 (NADSYN1)	0.94	0.73	0.69
AM071168	3-oxoacid CoA transferase 1 (OXCT1)	1.15	0.60	0.69
AM065353	Uncharacterised	0.84	0.82	0.69
AM067375	ribonuclease kappa	0.88	0.77	0.68
AM068817	Uncharacterised	0.95	0.71	0.68
AM063270	Putative methyltransferase (LOC424014)	0.92	0.74	0.68
AM071148	Ubiquitin-conjugating enzyme E2F (putative) (UBE2F)	0.93	0.74	0.68
AM065728	sperm-associated antigen 5-lik	0.84	0.81	0.68
AM066474	Hydroxyacylglutathione hydrolase-like (HAGHL)	0.95	0.71	0.68
AM069748	Polymerase (RNA) II (DNA directed) polypeptide H (POLR2H)	0.88	0.77	0.68
AM064152	Ubiquitin specific peptidase 48 (USP48)	0.82	0.83	0.68
AM069763	Microcephaly, primary autosomal recessive 1 (MCPH1)	0.80	0.85	0.68
AM068929	Dynactin 6 (DCTN6)	0.85	0.79	0.68
AM075531	Uncharacterised	0.86	0.79	0.68
AM063815	Centrin, EF-hand protein, 2 (CETN2)	0.96	0.70	0.67
AM066378	ras-related protein Rab-44-like	0.85	0.79	0.67
AM064149	GINS complex subunit 1 (Psf1 homolog) (GINS1)	1.11	0.60	0.67
AM067379	Uncharacterised	0.92	0.73	0.67
AM066618	serine/threonine-protein kinase WNK4-like	0.94	0.71	0.67
AM072072	Ring finger protein 126 (RNF126)	0.79	0.85	0.67
AM066175	protein jagunal homolog 1	0.84	0.80	0.67
AM063956	Mitochondrial fission process 1 (MTFP1)	0.93	0.72	0.67
AM066287	Cytoskeleton associated protein 2-like (CKAP2L)	0.75	0.89	0.67
AM063447	Heterogeneous nuclear ribonucleoprotein D-like (HNRPDL)	0.89	0.75	0.67

AM065237	Cytochrome P450, family 8, subfamily B, polypeptide 1 (CYP8B1)	0.79	0.84	0.67
AM072011	Protease, serine, 2 (trypsin 2) (PRSS2)	0.92	0.72	0.66
AM063678	Polymerase (DNA directed), epsilon 3 (p17 subunit) (POLE3)	0.86	0.77	0.66
AM067455	Crystallin, zeta (quinone reductase)-like 1 (CRYZL1)	0.84	0.79	0.66
AM065574	phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform isoform 2	0.87	0.76	0.66
AM066182	Uncharacterised	0.77	0.86	0.66
AM070744	DnaJ (Hsp40) homolog, subfamily C, member 15 (DNAJC15)	0.91	0.72	0.66
AM066242	ADP-ribosylation factor-like 3	0.87	0.76	0.66
BU133519	EPH receptor A2 (EPHA2)	0.94	0.71	0.66
AM065714	protein jagunal homolog 1	0.77	0.86	0.66
AM064897	Uncharacterised	0.71	0.92	0.66
AM069890	DNA polymerase delta subunit 2-like	0.93	0.71	0.66
AM065606	MEF2B neighbor (MEF2BNB)	0.97	0.68	0.66
AM066530	Uncharacterised	0.86	0.76	0.66
AM070725	Uncharacterised	0.92	0.71	0.66
AM066655	Ring finger protein 213 (RNF213)	0.95	0.69	0.65
AM072086	Deleted in primary ciliary dyskinesia homolog (mouse) (DPCD)	0.79	0.83	0.65
AM064451	Ring finger and CHY zinc finger domain containing 1 (RCHY1)	0.86	0.76	0.65
AM067655	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	0.85	0.77	0.65
AM071949	B-cell antigen receptor complex-associated protein alpha chain precursor	0.94	0.69	0.65
AM070239	Retinol saturase (all-trans-retinol 13,14-reductase) (RETSAT)	0.89	0.73	0.65
AM064802	Uncharacterised	0.91	0.71	0.65
AM067040	Cytochrome P450, family 51, subfamily A, polypeptide 1 (CYP51A1)	0.63	1.03	0.65
AM067495	Basic leucine zipper transcription factor, ATF-like (BATF)	0.91	0.71	0.65
AM068090	Uncharacterised	0.97	0.67	0.65
AM071198	Gem (nuclear organelle) associated protein 4 (GEMIN4)	0.72	0.90	0.65
AM071743	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM5)	0.81	0.81	0.65

AM070108	Brain protein 44-like (BRP44L)	0.89	0.73	0.65
AM075313	Uncharacterised	0.70	0.93	0.65
AM067309	RNA-binding protein with serine-rich domain 1	0.91	0.71	0.65
AM067066	N(alpha)-acetyltransferase 50, NatE catalytic subunit (NAA50)	0.90	0.72	0.65
AM070757	Sec61 alpha 1 subunit (S. cerevisiae) (SEC61A1)	0.69	0.94	0.65
AM064217	Uncharacterised	0.76	0.85	0.65
AM065080	Deoxyribonuclease I-like 3 (DNASE1L3)	0.98	0.66	0.65
AM064656	Uncharacterised	0.97	0.67	0.65
AM066116	Ubiquinol-cytochrome c reductase complex chaperone (UQCC)	0.76	0.84	0.65
AM064070	Tumor necrosis factor receptor superfamily, member 6b, decoy (TNFRSF6B)	0.98	0.66	0.65
AM071661	Adenosylhomocysteinase (AHCY)	0.94	0.69	0.64
AM066173	Peptidylprolyl isomerase E (cyclophilin E) (PPIE)	0.92	0.70	0.64
AM069849	Chemokine (C-X-C motif) receptor 4 (CXCR4)	1.08	0.60	0.64
AM072185	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1)	0.95	0.68	0.64
AM067352	germ cell-less protein-like 1	0.75	0.86	0.64
AM069783	Y box binding protein 1 (YBX1)	0.92	0.70	0.64
AM072004	Protein phosphatase 6, catalytic subunit (PPP6C)	0.83	0.77	0.64
AM066236	Uncharacterised LOC427029 (LOC427029)	0.66	0.97	0.64
AM063541	nuclear pore complex protein Nup160	0.80	0.79	0.64
AM070331	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (DDX17)	0.67	0.96	0.64
AM065955	Clathrin, light chain B (CLTB)	0.99	0.65	0.64
AM065175	Macrophage stimulating 1 (hepatocyte growth factor-like) (MST1)	0.91	0.70	0.64
AM064822	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1)	0.70	0.91	0.64
AM071889	tubulin alpha-1B chain	0.85	0.74	0.64

AM069206	Heterogeneous nuclear ribonucleoprotein R (HNRNPR)	0.85	0.75	0.64
AM063499	ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2)	0.78	0.81	0.63
AM068109	Uncharacterised	0.83	0.76	0.63
AM070716	leucine-rich repeat-containing protein 45	0.87	0.73	0.63
AM065819	probable phospholipid-transporting ATPase IG	0.76	0.83	0.63
AM063813	Uncharacterised	0.84	0.75	0.63
AM069568	Tubulin, beta 2C (TUBB2C)	0.90	0.70	0.63
AM069752	Acetyl-CoA acetyltransferase 1 (ACAT1)	0.95	0.66	0.63
AM070145	microspherule protein 1	0.89	0.71	0.63
AM068858	Small nuclear ribonucleoprotein polypeptide B (SNRPB2)	0.73	0.85	0.63
AM070677	Pentatricopeptide repeat domain 3 (PTCD3)	0.93	0.67	0.62
AM070849	TLC domain containing 1 (TLCD1)	0.83	0.75	0.62
AM067682	Replication protein A2, 32kDa (RPA2)	0.84	0.74	0.62
AM071776	nicotinamide riboside kinase 2-like	1.28	0.49	0.62
AM067475	Death associated protein 3 (DAP3)	0.81	0.77	0.62
AM066381	RAB19, member RAS oncogene family (RAB19)	0.85	0.73	0.62
AM066381	RAB19, member RAS oncogene family (RAB19)	0.91	0.68	0.62
AM071303	Solute carrier family 35, member B1 (SLC35B1)	0.82	0.75	0.62
AM070333	Uncharacterised	0.91	0.68	0.62
AM070730	Death associated protein 3 (DAP3)	0.77	0.80	0.62
AM067405	cytosol aminopeptidase	0.77	0.80	0.61
AM069745	RAN binding protein 1 (RANBP1)	0.75	0.82	0.61
AM069745	RAN binding protein 1 (RANBP1)	0.85	0.72	0.61
AM066092	Misato homolog 1 (Drosophila) (MSTO1)	0.74	0.83	0.61
AM065676	DnaJ (Hsp40) homolog, subfamily C, member 17 (DNAJC17)	0.82	0.75	0.61
AM066591	Nipped-B homolog (NIPBL)	0.86	0.71	0.61
AM066178	TRNA splicing endonuclease 2 homolog (S. cerevisiae) (TSEN2)	0.79	0.77	0.61

AM067711	Biphenyl hydrolase-like (serine hydrolase) (BPHL)	0.83	0.74	0.61
AM069665	Y box binding protein 1 (YBX1)	0.91	0.67	0.61
AM065862	Protein phosphatase 1, regulatory (inhibitor) subunit 8 (PPP1R8)	0.66	0.92	0.61
AM063783	Pyruvate kinase, muscle (PKM2)	0.82	0.74	0.61
AM066661	Chromatin accessibility complex 1 (CHRAC1)	0.77	0.78	0.61
AM071694	Small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3)	0.86	0.70	0.61
AM066433	Adhesion regulating molecule 1 (ADRM1)	0.86	0.70	0.61
AM064375	Lysine (K)-specific demethylase 5A (KDM5A)	1.20	0.51	0.61
AM066550	Kruppel-like factor 2 (lung) (KLF2)	0.73	0.83	0.61
AM070634	N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae) (NAA40)	0.94	0.64	0.61
AM070903	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 (PLOD2)	0.78	0.77	0.60
AM067071	Uncharacterised	0.84	0.72	0.60
AM075355	Uncharacterised	0.85	0.71	0.60
AM071721	Uncharacterised	0.73	0.83	0.60
AM065999	Phosphoglycerate mutase 1 (brain) (PGAM1)	0.92	0.66	0.60
AM065085	BCL2-associated athanogene 2 (BAG2)	0.82	0.74	0.60
AM071981	Lactate dehydrogenase B (LDHB)	0.79	0.77	0.60
AM070091	Heat shock 70kDa protein 9 (mortalin) (HSPA9)	0.77	0.78	0.60
AM066003	Uncharacterised LOC426097 (LOC426097)	0.90	0.67	0.60
AM066846	Splicing factor 3a, subunit 3, 60kDa (SF3A3)	0.78	0.77	0.60
AM066592	ATPase, H+ transporting, lysosomal V0 subunit a1 (ATP6V0A1)	0.99	0.61	0.60
AM065200	Etoposide induced 2.4 mRNA (EI24)	0.66	0.91	0.60
AM064835	NF-kappa-B inhibitor epsilon-like	0.84	0.72	0.60
AM065009	Regulator of G-protein signaling 5 (RGS5)	0.93	0.64	0.60
AM065525	Ras association (RalGDS/AF-6) domain family member 2 (RASSF2)	0.86	0.70	0.60
AM065171	RPE-spondin-like	0.67	0.90	0.60

AM066245	Proline synthetase co-transcribed homolog (bacterial) (PROSC)	0.81	0.73	0.60
AM071006	Acid phosphatase 1, soluble (ACP1)	0.96	0.62	0.60
AM071998	Cyclin Y-like 1 (CCNYL1)	0.90	0.66	0.60
AM066145	ADP-dependent glucokinase (ADPGK)	0.80	0.74	0.60
AM066108	Uncharacterised	0.96	0.62	0.60
AM065904	serine/threonine-protein kinase MARK2 isoform 2	0.52	1.15	0.60
AM069531	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1)	0.89	0.67	0.59
AM071077	Nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1 (NUDT16L1)	0.79	0.75	0.59
AM064609	V-myb myeloblastosis viral oncogene homolog (avian) (MYB)	1.16	0.51	0.59
AM069217	Uncharacterised	0.78	0.76	0.59
AM066144	Golgi to ER traffic protein 4 homolog (S. cerevisiae) (GET4)	0.95	0.62	0.59
AM071894	SEC62 homolog (S. cerevisiae) (SEC62)	0.84	0.70	0.59
AM067421	Histidine triad nucleotide binding protein 1 (HINT1)	0.72	0.83	0.59
AM066025	Mitochondrial carrier 2 (MTCH2)	0.96	0.61	0.59
AM069127	Histidyl-tRNA synthetase (HARS)	0.71	0.83	0.59
AM066001	RNA-binding protein with serine-rich domain 1	0.92	0.64	0.59
AM063585	Budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3)	0.83	0.71	0.59
AM063871	BRCA2 and CDKN1A interacting protein (BCCIP)	0.78	0.76	0.59
AM065330	Partner of NOB1 homolog (S. cerevisiae) (PNO1)	0.70	0.84	0.59
AM069303	Cysteine and glycine-rich protein 2 (CSRP2)	0.96	0.61	0.59
AM069439	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12)	0.70	0.84	0.58
AM070466	Proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2)	0.86	0.68	0.58

AM064832	Solute carrier family 19 (folate transporter), member 1 (SLC19A1)	0.74	0.78	0.58
AM065334	organic solute transporter subunit alpha-like	0.89	0.65	0.58
AM064298	proteasome subunit beta type-6	0.80	0.72	0.58
AM065940	Rho GTPase activating protein 19 (ARHGAP19)	0.85	0.68	0.58
AM065755	Histone deacetylase 8 (HDAC8)	0.86	0.67	0.58
AM072094	Heat shock 70kDa protein 8 (HSPA8)	0.86	0.67	0.58
AM071236	39S ribosomal protein L2, mitochondrial	0.84	0.68	0.57
AM068863	microspherule protein 1	0.84	0.68	0.57
AI982046	TNF RECEPTOR ASSOCIATED FACTOR 1 (TRAF1)	0.79	0.72	0.57
AM065351	Uncharacterised	0.95	0.60	0.57
AM075536	Uncharacterised	0.83	0.68	0.57
AM066159	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	0.73	0.77	0.56
AM066027	Mitochondrial amidoxime reducing component 2 (MARC2)	0.87	0.64	0.56
AM069085	Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2)	0.83	0.68	0.56
AM068150	Protein disulfide isomerase family A, member 6 (PDIA6)	0.73	0.76	0.56
AM065760	Patched 1 (PTCH1)	0.85	0.65	0.56
AM063986	Small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB)	0.79	0.70	0.56
AM071781	Lectin, galactoside-binding, soluble, 3 (LGALS3)	1.21	0.46	0.56
AM075570	Uncharacterised	0.82	0.68	0.56
AM063427	general transcription factor 3C polypeptide 2	0.93	0.60	0.55
AM067636	ubiquitin carboxyl-terminal hydrolase 42	0.94	0.59	0.55
AM065891	cleavage and polyadenylation specificity factor subunit 5	0.88	0.63	0.55
AM067023	Progressive external ophthalmoplegia 1 (C6H10orf2)	0.78	0.70	0.55
AM064120	WD repeat domain 43 (WDR43)	0.74	0.75	0.55
AM069834	Replication factor C (activator 1) 2, 40kDa (RFC2)	0.91	0.60	0.55
AM063936	clone ChAcyl-CoA thioesterase 13 (ACOT13) EST990f10	0.60	0.91	0.55
AM067692	Uncharacterised	0.81	0.68	0.55
AM071794	Uncharacterised	0.88	0.62	0.55

AM065835	Structure specific recognition protein 1 (SSRP1)	0.87	0.62	0.54
AM065886	N(alpha)-acetyltransferase 25, NatB auxiliary subunit (NAA25)	0.80	0.68	0.54
AM065082	peroxisomal N(1)-acetyl-spermine/spermidine oxidase-like	0.80	0.68	0.54
AM066813	acyl-CoA synthetase family member 2, mitochondrial	0.82	0.66	0.54
AM069779	pumilio domain-containing protein C14orf21 homolog	0.84	0.64	0.54
AM065841	Queuine tRNA-ribosyltransferase domain containing 1 (QTRTD1)	0.87	0.62	0.54
AM064943	PROTEIN: receptor-type tyrosine-protein kinase FLT3-like	0.78	0.69	0.54
AM065821	Protein kinase C, delta	0.51	1.05	0.54
AM075321	Uncharacterised	0.89	0.61	0.54
AM068117	plasma cell-induced resident endoplasmic reticulum protein-like	0.85	0.63	0.54
AM068773	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A (PRPF38A)	0.88	0.61	0.54
AM065605	Uncharacterised	0.72	0.74	0.53
AM067207	Annexin A6 (ANXA6)	0.86	0.62	0.53
AM071803	Zinc finger, matrin type 5 (ZMAT5)	0.70	0.76	0.53
AM066678	Uncharacterised	0.92	0.58	0.53
AM068185	Carboxylesterase 1 (monocyte/macrophage serine esterase 1) (CES1)	0.90	0.59	0.53
AM063336	Vacuolar protein sorting 24 homolog (S. cerevisiae) (VPS24)	0.80	0.66	0.53
AM063729	Signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3)	0.85	0.62	0.53
AM071012	Processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae) (POP5)	0.92	0.57	0.53
AM067359	Ddx49-ADEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (DDX49) -prov protein	0.61	0.86	0.53
AM063749	CAD protein	0.89	0.59	0.52
AM066230	farnesyl pyrophosphate synthase	0.79	0.66	0.52
AM064023	WD repeat-containing protein 3	0.69	0.76	0.52
AM067047	Gephyrin (GPHN)	0.84	0.62	0.52
AM068974	SLAM family member 8-like	0.92	0.56	0.52
AM067991	Eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa (EIF2S1)	0.89	0.58	0.52
AM065547	Uncharacterised	0.90	0.57	0.52
AM064711	RAB11A, member RAS oncogene family (RAB11A)	0.75	0.69	0.52

AM064079	Serine peptidase inhibitor, Kazal type 5 (SPINK5)	0.70	0.74	0.52
AM064640	LOW QUALITY PROTEIN: GPI transamidase component PIG-T-like	0.85	0.61	0.52
AM067063	U3 small nucleolar RNA-interacting protein 2	0.73	0.71	0.52
AM065589	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa (NDUFA5)	0.73	0.70	0.51
AM066313	Cystatin C (CST3)	0.77	0.66	0.51
AM070094	torsin-1B	0.70	0.72	0.51
AM069516	Phosphatidylethanolamine binding protein 1 (PEBP1)	0.73	0.69	0.51
AM066070	small subunit processome component 20 homolog	0.85	0.60	0.51
AM064767	Family with sequence similarity 96, member A (FAM96A)	0.80	0.63	0.51
AM070410	Signal sequence receptor, alpha (SSR1)	0.75	0.67	0.50
AM067439	MAK16 homolog (S. cerevisiae) (MAK16)	0.77	0.65	0.50
AM066914	BTB/POZ domain-containing protein KCTD3	0.75	0.67	0.50
AM071790	coiled-coil domain-containing protein 71-like	0.74	0.67	0.50
AM071846	Mu immunoglobulin heavy chain C region	0.78	0.64	0.50
AM064653	Cytokine receptor-like factor 3 (CRLF3)	0.78	0.63	0.50
AM065149	Mannosidase, alpha, class 1B, member 1 (MAN1B1)	0.78	0.63	0.49
AM068044	Peptidylprolyl isomerase B (cyclophilin B) (PPIB)	0.81	0.61	0.49
AM066719	FtsJ homolog 3 (E. coli) (FTSJ3)	0.65	0.76	0.49
AM071539	ADP-ribosylation factor-like 1 (ARL1)	0.77	0.63	0.49
AM065433	Uncharacterised	0.87	0.56	0.49
AM063885	Cyclin-dependent kinase 1 (CDK1)	0.92	0.53	0.49
AM070689	glutathione S-transferase omega-1 isoform 2	0.76	0.64	0.49
AM064370	LYR motif containing 5 (LYRM5)	0.72	0.68	0.48
AM070721	tubulin alpha-1B chain	0.80	0.60	0.48
AM067279	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM7)	0.68	0.70	0.48
AM070678	peptidyl-prolyl cis-trans isomerase H	0.83	0.58	0.48
AM065852	Tropomodulin 1 (TMOD1)	0.62	0.77	0.47

AM063132	tubulin-folding cofactor B	0.73	0.64	0.47
AM068695	serine/arginine-rich splicing factor 2	0.88	0.54	0.47
AM068088	Uncharacterised	0.76	0.62	0.47
AM064344	Proliferating cell nuclear antigen (PCNA)	0.91	0.52	0.47
AM068994	Ribonucleotide reductase M2 (RRM2)	0.90	0.52	0.47
AM066363	heparan-alpha-glucosaminide N-acetyltransferase	0.65	0.72	0.47
AM065943	Dynein, light chain, Tctex-type 1 (DYNLT1)	0.85	0.54	0.46
AM064778	Ribonucleotide reductase M1 (RRM1)	0.94	0.49	0.46
AM065324	Uncharacterised	0.81	0.56	0.46
AM065850	Ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase) (USP14)	0.70	0.65	0.45
AM069986	RAN, member RAS oncogene family (RAN)	0.74	0.61	0.45
AM071746	Thymosin beta 15 (LOC100502566)	0.79	0.57	0.45
AM068181	tubulin alpha-4A chain	0.70	0.64	0.45
AM072144	Chaperonin containing TCP1, subunit 7 (eta) (CCT7)	0.67	0.67	0.45
AM066564	Isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae) (IAH1)	0.59	0.75	0.45
AM066478	Leucine rich repeat and sterile alpha motif containing 1 (LRSAM1)	0.73	0.59	0.43
AM067252	Uncharacterised	0.78	0.54	0.42
AM063638	thimet oligopeptidase-like	0.66	0.64	0.42
AM065980	thimet oligopeptidase-like	0.75	0.55	0.41
AM070961	SLAM family member 8-like	1.08	0.38	0.41
AM069279	Heat shock 70kDa protein 8 (HSPA8)	0.77	0.53	0.40
AM063229	Heat shock 70kDa protein 8 (HSPA8)	0.64	0.62	0.40
AM065982	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 2 (SLC28A2)	0.77	0.51	0.40
AM072018	MHC class II beta chain (BLB2)	0.85	0.46	0.39
AM069616	Nuclear distribution gene C homolog (A. nidulans) (NUDC)	0.63	0.61	0.39
AM066709	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3)	0.70	0.55	0.39
AM068108	Uncharacterised	0.31	1.23	0.38
AM066237	Chaperonin containing TCP1, subunit 4 (delta)	0.73	0.50	0.37
AM071140	Small nuclear ribonucleoprotein polypeptide E (snRNP-E)	0.80	0.45	0.36
AM069195	Heat shock protein 70kDa beta protein 8	0.63	0.54	0.34
AM068465	nucleophosmin/nucleoplasmin 3	0.62	0.48	0.29
AM064397	Heat shock protein 90kDa beta (Grp94), member 1	0.49	0.59	0.29

Overlapped genes at 48 and 72 h

Genbank	Name	Gene symbol	FoldChange 48 h	Fold Change 72 h
AM071288	PREDICTED: normal mucosa of esophagus-specific gene 1 protein-like isoform 1	NMES1	2.11	-1.59
AM069035	protein FAM60A	FAM60A	1.87	-1.56
AM063713	nuclear casein kinase and cyclin-dependent kinase substrate 1 (NUCKS1, JC7, NUCKS)	NUCKS1	1.82	1.82
AM075540	No blast file found		1.81	-1.64
AM067693	death effector domain containing	DEDD	1.67	1.55
AM067846	Glyceraldehyde 3-phosphate dehydrogenase	GAPDH	1.61	-1.56
AM071638	LOC417345	LOC417345	1.54	-1.51
AM069195	heat shock 70kDa protein 8 (HSPA8, HSC70)	HSPA8	1.50	2.19
AM065739	solute carrier family 7 (amino acid transporter light chain, L system), member 5	SLC7A5	-1.55	-1.76
AM072025	YTH domain containing 1	YTHDC1	-1.58	-1.58
AM066657	Meis homeobox 1	MEIS1	-1.70	-1.94
AM069042	high mobility group protein HMGI-C-like	HMGI-C	-1.78	-1.66
AM068392	uncharacterized LOC107052719, transcript variant X1	LOC107052719	-1.81	-1.68
AM065719	transmembrane protein 86A	TMEM86A	-1.91	-2.62
AM066521	sulfotransferase family cytosolic 2B member 1-like	SULT2B1	-2.10	-1.81
AM066655	ring finger protein 213	RNF213	-2.53	-1.88
AM067376	coiled-coil domain containing 50	CCDC50	-4.02	-3.22
AM070526	lymphocyte-specific protein 1	LSP1	-4.73	-2.11

Ingenuity Pathway analysis
Biological function analysis (48 h)

Category	Time	P. Value	Transcripts	Transcripts
Cell-To-Cell Signaling and Interaction	48h	2.43E-04-4.77E-02	IFRD1,PTBP1,TGFBI,APOA1,PPBP,PTGS1,COL2A1 (includes EG:1280),LY6E,VAV1,GRIK2,CARD11,NID1	12
Tissue Development	48h	2.69E-04-4.77E-02	IFRD1,PTBP1,TGFBI,APOA1,PPBP,PTGS1,COL2A1 (includes EG:1280),LY6E,VAV1,CARD11,NID1	11
Organismal Development	48h	7.8E-04-4.77E-02	IFRD1,TGFBI,APOA1,PTGS1,COL2A1 (includes EG:1280),LY6E,ABCC10,GRIK2,NID1,VGLL1	10
Immunological Disease	48h	5.88E-04-4.94E-02	TRAK2,FDPS,AP4B1,CNN3,APOA1,PPBP,PTGS1,COL2A1 (includes EG:1280),VAV1,CARD11	10
Molecular Transport	48h	2.84E-04-4.91E-02	IFRD1,AP4B1,APOA1,PTGS1,PPBP,SLC7A5,LY6E,VAV1,GRIK2,ATP11B	10
Small Molecule Biochemistry	48h	2.84E-04-4.77E-02	IFRD1,FDPS,APOA1,PPBP,PTGS1,COL2A1 (includes EG:1280),LY6E,SLC7A5,ATP11B	9
Inflammatory Disease	48h	6.49E-04-4.6E-02	FDPS,TRAK2,CNN3,APOA1,PTGS1,COL2A1 (includes EG:1280),LY6E,CARD11	8
Tissue Morphology	48h	4.74E-03-4.6E-02	TGFBI,APOA1,PTGS1,COL2A1 (includes EG:1280),VAV1,ABCC10,CARD11,NID1	8
Hematological System Development and Function	48h	2.69E-04-4.43E-02	TGFBI,APOA1,PTGS1,PPBP,ABCC10,VAV1,GRIK2,CARD11	8
Embryonic Development	48h	7.8E-04-4.77E-02	IFRD1,APOA1,PTGS1,COL2A1 (includes EG:1280),LY6E,VAV1,NID1	7
Cell Signaling	48h	5.41E-03-3.03E-02	APOA1,PTGS1,CXXC5,PPBP,VAV1,GRIK2,CARD11	7
Inflammatory Response	48h	2.43E-04-4.77E-02	APOA1,PTGS1,PPBP,COL2A1 (includes EG:1280),VAV1,GRIK2,CARD11	7
Hereditary Disorder	48h	1.81E-03-4.6E-02	FLOT2,TGFBI,APOA1,PTGS1,PPBP,COL2A1 (includes EG:1280),GRIK2	7
Infectious Disease	48h	5.88E-04-4.4E-02	FDPS,FLOT2,PPBP,PTGS1,VAV1,RRAGD	6
Developmental Disorder	48h	1.81E-03-4.94E-02	FDPS,FLOT2,TGFBI,APOA1,PTGS1,COL2A1 (includes EG:1280)	6
Lipid Metabolism	48h	1.81E-03-4.77E-02	IFRD1,FDPS,APOA1,PPBP,PTGS1,ATP11B	6
Cardiovascular System Development and Function	48h	1.81E-03-4.6E-02	TGFBI,APOA1,PPBP,PTGS1,VAV1,NID1	6
Cellular Function and Maintenance	48h	1.81E-03-4.08E-02	APOA1,PTGS1,PPBP,VAV1,GRIK2,CARD11	6
Cell Death	48h	1.81E-03-3.21E-02	PPBP,PTGS1,VAV1,ABCC10,GRIK2,CARD11	6
Organ Development	48h	7.8E-04-4.77E-02	IFRD1,APOA1,COL2A1 (includes EG:1280),LY6E,NID1	5
Dermatological Diseases and Conditions	48h	5.41E-03-4.08E-02	CNN3,APOA1,PTGS1,COL2A1 (includes EG:1280),CARD11	5
Cell Morphology	48h	5.3E-04-4.6E-02	IFRD1,PTBP1,TGFBI,VAV1,CARD11	5
Hematological Disease	48h	3.61E-03-3.56E-02	FDPS,APOA1,PTGS1,VAV1,GRIK2	5
Cellular Development	48h	2.72E-03-4.6E-02	IFRD1,APOA1,PTGS1,VAV1,CARD11	5

Lymphoid Tissue Structure and Development	48h	2.72E-03-4.08E-02	TGFBI,PTGS1,ABCC10,VAV1,CARD11	5
Ophthalmic Disease	48h	1.81E-03-4.94E-02	TGFBI,APOA1,PTGS1,PPBP,COL2A1 (includes EG:1280)	5
Metabolic Disease	48h	1.81E-03-4.6E-02	FDPS,FLOT2,TGFBI,APOA1,PTGS1	5
Cellular Growth and Proliferation	48h	1.81E-03-4.08E-02	APOA1,PPBP,VAV1,RCHY1,CARD11	5
Respiratory System Development and Function	48h	1.81E-03-3.61E-03	PTGS1,COL2A1 (includes EG:1280)	5
Cellular Assembly and Organization	48h	1.81E-03-3.38E-02	TRAK2,PTBP1,APOA1,COL2A1 (includes EG:1280),VAV1	5
Respiratory Disease	48h	1.81E-03-3.21E-02	FLOT2,TGFBI,PTGS1,COL2A1 (includes EG:1280),RRAGD	5
Psychological Disorders	48h	1.4E-02-4.43E-02	FDPS,APOA1,PPBP,GRIK2,NID1	5
Gastrointestinal Disease	48h	5.41E-03-4.94E-02	APOA1,PPBP,PTGS1,COL2A1 (includes EG:1280)	4
Renal and Urological Disease	48h	5.41E-03-3.56E-02	FDPS,APOA1,PTGS1,COL2A1 (includes EG:1280)	4
Hematopoiesis	48h	5.3E-04-4.6E-02	APOA1,PTGS1,VAV1,CARD11	4
Organismal Functions	48h	4.71E-03-1.79E-02	PPBP,PTGS1,COL2A1 (includes EG:1280),GRIK2	4
Vitamin and Mineral Metabolism	48h	3.61E-03-3.9E-02	FDPS,APOA1,PPBP,VAV1	4
Drug Metabolism	48h	2.84E-04-4.08E-02	PTGS1,SLC7A5,LY6E,CARD11	4
Antigen Presentation	48h	2.43E-04-4.77E-02	APOA1,PPBP,VAV1,CARD11	4
Skeletal and Muscular System Development and Function	48h	1.81E-03-4.77E-02	IFRD1,COL2A1 (includes EG:1280),LY6E,VGLL1	4
Cellular Compromise	48h	1.81E-03-4.6E-02	TGFBI,PPBP,SLC7A5,VAV1	4
Cardiovascular Disease	48h	1.81E-03-4.43E-02	APOA1,PTGS1,COL2A1 (includes EG:1280),GRIK2	4
Cellular Movement	48h	1.08E-02-4.06E-02	TGFBI,APOA1,PPBP,COL2A1 (includes EG:1280)	4
Cell Cycle	48h	7.21E-03-4.77E-02	TGFBI,VAV1,RCHY1	3
Endocrine System Disorders	48h	7.21E-03-4.01E-02	APOA1,CXXC5,PTGS1	3
Organismal Injury and Abnormalities	48h	5.41E-03-4.94E-02	APOA1,PTGS1,COL2A1 (includes EG:1280)	3
Connective Tissue Development and Function	48h	5.41E-03-4.77E-02	TGFBI,PPBP,COL2A1 (includes EG:1280)	3
Immune Cell Trafficking	48h	2.69E-04-3.73E-02	APOA1,PPBP,VAV1	3
Nervous System Development and Function	48h	1.81E-03-4.94E-02	IFRD1,COL2A1 (includes EG:1280),GRIK2	3
Cell-mediated Immune Response	48h	1.81E-03-4.08E-02	PTGS1,VAV1,CARD11	3
Protein Synthesis	48h	9.37E-03-3.73E-02	VAV1,CARD11	2
Tumor Morphology	48h	9.01E-03-3.21E-02	TGFBI,VAV1	2
Endocrine System Development and Function	48h	7.8E-04-3.9E-02	APOA1,LY6E	2
Digestive System Development and Function	48h	5.41E-03-5.41E-03	IFRD1,PTGS1	2
Hepatic System Disease	48h	5.41E-03-5.41E-03	APOA1,PTGS1	2

Reproductive System Development and Function	48h	5.41E-03-4.43E-02	PTGS1,SLC7A5	2
Reproductive System Disease	48h	5.41E-03-4.01E-02	CXXC5,PTGS1	2
Free Radical Scavenging	48h	3.61E-03-4.6E-02	PPBP,PTGS1	2
Energy Production	48h	3.61E-03-4.3E-02	APOA1,PTGS1	2
Post-Translational Modification	48h	3.56E-02-4.25E-02	TRAK2,RCHY1	2
Visual System Development and Function	48h	3.25E-03-4.43E-02	TGFBI,COL2A1 (includes EG:1280),NID1	2
RNA Post-Transcriptional Modification	48h	2.67E-02-2.67E-02	PTBP1,HNRNPA0	2
Cellular Response to Therapeutics	48h	2.46E-02-2.46E-02	PTGS1,RCHY1	2
Humoral Immune Response	48h	2.43E-04-4.43E-02	VAV1,CARD11	2
Carbohydrate Metabolism	48h	1.81E-03-4.77E-02	APOA1,COL2A1 (includes EG:1280)	2
Renal and Urological System Development and Function	48h	1.08E-02-3.73E-02	PTGS1,NID1	2
Dental Disease	48h	5.41E-03-5.41E-03	COL2A1 (includes EG:1280)	1
Hepatic System Development and Function	48h	5.41E-03-5.41E-03	PTGS1	1
Gene Expression	48h	3.61E-03-3.61E-03	VAV1	1
DNA Replication, Recombination, and Repair	48h	3.38E-02-3.38E-02	TGFBI	1
Hair and Skin Development and Function	48h	2.5E-02-2.5E-02	TGFBI	1
Amino Acid Metabolism	48h	1.81E-03-2.15E-02	SLC7A5	1

Ingenuity Pathway analysis
Biological function analysis (72 h)

Category	Time	P.Value	Transcripts	Transcripts
Cell Death	72h	6.72E-06-1.89E-02	CD247,PSMA3,LGALS3,CLN8,LIMK2,KRAS,EIF2S1,DTYMK,CCT4,PTPRC,CTSD,CST3,ANXA5,DLST,DAP3,ADA,UNG,MVP,TP53INP1,STXBP1,ADRM1,TIA1,RRM2,IFNGR2,STAT3,SSRP1,XPA,CDK1,RRM1,HSPA8,TMEM57,ITGB2,PCNA,RASSF2,PRELID1,SATB1,LSP1 (includes EG:16985),CCT7,ZYX,NAGLU,CAPN2,FEN1,HHEX,MAP3K3,TK1	45
Cellular Growth and Proliferation	72h	5.36E-04-1.74E-02	CD247,LGALS3,INSIG1,GRIA1,RAN,KRAS,NUDC,DTYMK,PTPRC,CTSD,IMPDH2,CST3,DLST,DAP3,IFI30,ADA,MVP,MCM5,TP53INP1,RRM2,STAT3,CDK1,XPA,RRM1,HSPA8,ITGB2,PCNA,NASP,SATB1,CCT7,ZYX,CAPN2,FEN1,HHEX,MAP3K3	35
Immunological Disease	72h	4.55E-06-1.71E-02	CD247,KRAS,PTPRC,CTSD,KCTD20,IMPDH2,LSM7,CST3,ANXA5,PNRC1,ADA,IFI30,SNRPD3,UNG,ATP1B1,IFNGR2,RRM2,STAT3,CD3D,CDK1,RRM1,HSPA8,ITGB2,PCNA,SATB1,NAA25,ZYX,SEC62 (includes EG:294912),FEN1,TK1	30
Tissue Morphology	72h	9.23E-05-1.87E-02	CD247,LGALS3,GRIA1,KRAS,COL5A1,PTPRC,CTSD,IMPDH2,CST3,IFI30,ADA,ACTG2,UNG,TP53INP1,TIA1,FEZ1,SLA,STAT3,SSRP1,CD3D,XPA,ITGB2,SATB1,LSP1 (includes EG:16985),NAGLU,FEN1,HHEX,TK1	28

Cellular Function and Maintenance	72h	5.7E-05-1.9E-02	CD247,LGALS3,CLN8,RAN,KRAS,PTPRC,COL5A1,IMPDH2,CST3,ANXA5,IFI30,ADA,STXBP1,TIA1,SLA,IFNGR2,STAT3,CD3D,SSRP1,XPA,CDK1,ITGB2,PCNA,LSP1 (includes EG:16985),SATB1,PRELID1,NAGLU	27
Hematological System Development and Function	72h	6.94E-05-1.9E-02	CD247,LGALS3,KRAS,PTPRC,CTSD,IMPDH2,ANXA5,ADA,IFI30,MVP,TP53INP1,TIA1,SLA,IFNGR2,STAT3,CD3D,XPA,HSPA8,ITGB2,PCNA,SATB1,PRELID1,LSP1 (includes EG:16985),NAGLU,HHEX	25
Cellular Development	72h	6.94E-05-1.88E-02	CD247,TP53INP1,LGALS3,ATP1B1,FEZ1,SLA,RRM2,IFNGR2,LIMK2,KRAS,STAT3,CD3D,CDK1,PTPRC,HSPA8,CTSD,ITGB2,IMPDH2,SATB1,PRELID1,ADA,HHEX,MAP3K3,MVP	24
Cell Morphology	72h	8.1E-04-1.89E-02	CD247,LGALS3,FEZ1,GRIA1,SLA,RRM2,KRAS,LIMK2,STAT3,XPA,PTPRC,ITGB2,CTSD,PCNA,IMPDH2,ANXA5,LSP1 (includes EG:16985),ADA,NAGLU,ZYX,CAPN2,FEN1,HHEX	23
Small Molecule Biochemistry	72h	2.9E-05-1.9E-02	ACAT2,INSIG1,RRM2,STAT3,DTYMK,CDK1,XPA,RRM1,HSPA8,CETN2,CTSD,PCNA,UGDH,IMPDH2,ANXA5,DLST,ADA,NAGLU,LSS,TK1,UNG,MVP	22
Tissue Development	72h	1.93E-04-1.88E-02	CD247,STXBP1,LGALS3,ATP1B1,KRAS,STAT3,CD3D,EGFL7,XPA,PTPRC,COL5A1,ITGB2,CTSD,ANXA5,SATB1,ADA,ZYX,NAGLU,FEN1,CAPN2,NIPBL,HHEX	22
Cellular Assembly and Organization	72h	4.79E-04-1.9E-02	STXBP1,LGALS3,CLN8,FEZ1,GRIA1,RAN,KRAS,SSRP1,CDK1,XPA,HSPA8,COL5A1,CTSD,CETN2,CST3,ANXA5,SATB1,ADA,ZYX,NAGLU,AKAP9	21

Organismal Survival	72h	3.15E-03-3.15E-03	TP53INP1,LGALS3,ATP1B1,TIA1,INSIG1,STAT3,SSRP1,EGFL7,PTPRC,COL5A1,ITGB2,CTSD,NASP,CST3,ADA,NAGLU,CAPN2,FEN1,MAP3K3,UNG,TK1	21
Infectious Disease	72h	9.69E-05-1.71E-02	CD247,STXBP1,PSMA3,RRM2,NUP214,LIMK2,STAT3,RPL10A,PTPRC,COL5A1,ITGB2,P2RY10,IMPDH2,PNRC1,DLST,PSMA5,LSP1 (includes EG:16985),ADA,ZYX,SNRPD3	20
Cell Cycle	72h	2.19E-04-1.8E-02	TP53INP1,LGALS3,RAN,NUP214,KRAS,STAT3,DTYMK,SSRP1,XPA,CDK1,RRM1,HSPA8,PTPRC,CETN2,NASP,PCNA,RASSF2,CAPN2,HHEX,AKAP9	20
Embryonic Development	72h	1.93E-04-1.71E-02	CD247,TP53INP1,ATP1B1,KRAS,STAT3,CD3D,SSRP1,XPA,COL5A1,PTPRC,CTSD,ITGB2,SATB1,DLST,DAP3,ADA,NAGLU,FEN1,NIPBL,HHEX	20
Inflammatory Response	72h	1.19E-04-1.9E-02	CD247,TP53INP1,LGALS3,IFNGR2,KRAS,STAT3,CD3D,XPA,PTPRC,CTSD,ITGB2,IMPDH2,CST3,ANXA5,LSP1 (includes EG:16985),SATB1,ADA,NAGLU,FEN1,TK1	20
Organismal Development	72h	1.93E-04-1.71E-02	CD247,LGALS3,ATP1B1,KRAS,STAT3,CD3D,XPA,COL5A1,PTPRC,CTSD,ITGB2,CST3,SATB1,ADA,NAGLU,FEN1,NIPBL,HHEX,ACTG2	19
Respiratory Disease	72h	1.71E-05-1.73E-02	LGALS3,IFNGR2,RRM2,KRAS,STAT3,EGFL7,CDK1,XPA,RRM1,PTPRC,ITGB2,CTSD,PCNA,IMPDH2,ANXA5,IFI30,ADA,UNG,TK1	19
Reproductive System Disease	72h	8.92E-05-1.71E-02	MCM5,TP53INP1,IFNGR2,RRM2,LRSAM1,KRAS,STAT3,SSRP1,EGFL7,CDK1,RRM1,PTPRC,PCNA,UGDH,KHDRBS3,ADA,IFI30,TK1	18

Protein Synthesis	72h	7.22E-04-5.72E-03	STXBP1,ADRM1,CLN8,TIA1,RRM2,LRSAM1,MAN1B1,BAG2,EIF2S1,RRM1,PTPRC,CTSD,IMPDH2,CST3,IFI30,NAGLU,CAPN2,TK1	18
DNA Replication, Recombination, and Repair	72h	4.03E-05-1.8E-02	TIA1,SLA,RRM2,RAN,SSRP1,XPA,CDK1,RRM1,CETN2,PCNA,NASP,CST3,ADA,FEN1,CAPN2,AKAP9,TK1,UNG	18
Hematological Disease	72h	1.92E-06-1.71E-02	CD247,RNF213,RRM2,NUP214,KRAS,STAT3,CDK1,RRM1,PTPRC,ITGB2,PCNA,IMPDH2,PNRC1,SATB1,ADA,FEN1,SNRPD3,UNG	18
Inflammatory Disease	72h	1.72E-03-1.75E-02	MCM5,CD247,TP53INP1,TIA1,IFNGR2,KRAS,STAT3,CD3D,PTPRC,HSPA8,ITGB2,KCTD20,CST3,NAA25,NAGLU,SEC62 (includes EG:294912),CAPN2,MAP3K3	18
Molecular Transport	72h	9.69E-05-1.9E-02	DYNLT1,STXBP1,ACAT2,RRM2,RAN,NUP214,KRAS,STAT3,HSPA8,CTSD,PCNA,ANXA5,ARF4,ADA,NAGLU,HHEX,MVP	17
Lymphoid Tissue Structure and Development	72h	8.33E-05-1.88E-02	CD247,LGALS3,SLA,IFNGR2,KRAS,STAT3,CD3D,PTPRC,ITGB2,CTSD,IMPDH2,PRELID1,SATB1,ADA,MAP3K3,UNG,TK1	17
Skeletal and Muscular Disorders	72h	2.23E-03-1.71E-02	MCM5,CD247,TIA1,IFNGR2,STAT3,CD3D,COL5A1,PTPRC,HSPA8,ITGB2,KCTD20,CST3,NAA25,NAGLU,SEC62 (includes EG:294912),CAPN2,MAP3K3	17
Cell-To-Cell Signaling and Interaction	72h	1.93E-04-1.71E-02	CD247,STXBP1,LGALS3,GRIA1,KRAS,STAT3,CD3D,EGFL7,PTPRC,ITGB2,IMPDH2,CST3,ANXA5,SATB1,ADA,ZYX,CAPN2	17
Endocrine System Disorders	72h	1.77E-04-1.71E-02	TP53INP1,LGALS3,RRM2,IFNGR2,LRSAM1,KRAS,STAT3,SSRP1,CDK1,RRM1,PTPRC,CTSD,PCNA,LSM7,CST3,DAP3,IFI30	17

Hematopoiesis	72h	6.94E-05-1.88E-02	CD247,LGALS3,SLA,IFNGR2,KRAS,STAT3,CD3D,PTPRC,CTSD,ITGB2,IMPDH2,LSP1 (includes EG:16985),PRELID1,SATB1,ADA,HHEX	16
Connective Tissue Disorders	72h	2.23E-03-1.71E-02	MCM5,CD247,TIA1,STAT3,CD3D,COL5A1,PTPRC,HSPA8,ITGB2,KCTD20,CST3,NAA25,NAGLU,SEC62 (includes EG:294912),CAPN2,MAP3K3	16
Organ Development	72h	1.93E-04-1.45E-02	CD247,INSIG1,KRAS,STAT3,CD3D,XPA,PTPRC,COL5A1,ITGB2,CTSD,SATB1,ADA,NAGLU,NIPBL,HHEX,TK1	16
Organismal Injury and Abnormalities	72h	9.69E-05-1.14E-02	STXBP1,PSMA3,NUP214,KRAS,LIMK2,STAT3,RPL10A,COL5A1,ITGB2,CST3,PSMA5,ADA,ZYX,SNRPD3,UNG	15
Developmental Disorder	72h	1.65E-03-1.72E-02	CD247,LGALS3,CLN8,KRAS,STAT3,XPA,COL5A1,PTPRC,CTSD,CST3,ADA,NAGLU,NIPBL,HHEX,TK1	15
Renal and Urological Disease	72h	1.31E-04-4.29E-03	STXBP1,PSMA3,RRM2,NUP214,KRAS,LIMK2,STAT3,RPL10A,RRM1,COL5A1,CST3,PSMA5,NAGLU,ZYX,SNRPD3	15
Nucleic Acid Metabolism	72h	2.9E-05-1.71E-02	RRM2,STAT3,DTYMK,XPA,CDK1,RRM1,CETN2,PCNA,UGDH,IMPDH2,DLST,ADA,UNG,TK1	14
Organ Morphology	72h	3.23E-04-1.87E-02	CD247,KRAS,STAT3,XPA,PTPRC,CTSD,ITGB2,SATB1,ADA,NAGLU,HHEX,TK1,UNG	13
Digestive System Development and Function	72h	1.93E-04-1.33E-02	TP53INP1,KRAS,STAT3,XPA,PTPRC,CTSD,ITGB2,ADA,NAGLU,FEN1,NIPBL,HHEX,TK1	13
Post-Translational Modification	72h	7.3E-04-7.54E-03	HSPA8,CCT4,PTPRC,CTSD,ADRM1,IMPDH2,CST3,RRM2,CAPN2,BAG2,TK1,RRM1	12
Hepatic System Disease	72h	4.14E-03-1.71E-02	HSPA8,ITGB2,CTSD,ACAT2,CST3,PNRC1,RAN,RRM2,KRAS,STAT3,BAG2,XPA	12

Visual System Development and Function	72h	4.36E-04-1.45E-02	CD247,COL5A1,CTSD,ITGB2,LGALS3,NAGLU,KRAS,NIPBL,STAT3,AKAP9,XPA	11
Immune Cell Trafficking	72h	1.93E-04-1.9E-02	CD247,PTPRC,ITGB2,IMPDH2,LGALS3,ANXA5,LSP1 (includes EG:16985),SATB1,ADA,STAT3,CD3D	11
Cellular Movement	72h	1.93E-04-1.9E-02	PTPRC,CTSD,ITGB2,LGALS3,ANXA5,LSP1 (includes EG:16985),RRM2,CAPN2,STAT3,SSRP1,AKAP9	11
Cardiovascular Disease	72h	1.11E-02-1.71E-02	CTSD,ITGB2,PCNA,LGALS3,ACAT2,CST3,ANXA5,RNF213,STAT3,TK1,UNG	11
Cell-mediated Immune Response	72h	8.33E-05-1.88E-02	CD247,PTPRC,ITGB2,SLA,PRELID1,SATB1,ADA,IFNGR2,STAT3,CD3D	10
Protein Degradation	72h	7.22E-04-5.72E-03	PTPRC,CTSD,STXBP1,ADRM1,CST3,IFI30,NAGLU,LRSAM1,CAPN2,MAN1B1	10
Cellular Compromise	72h	5.72E-03-1.71E-02	PTPRC,CTSD,ITGB2,GRIA1,ANXA5,PGAM1,RRM2,NAGLU,XPA,UNG	10
Hepatic System Development	72h	1.93E-04-1.33E-02	PTPRC,ITGB2,ADA,NAGLU,NIPBL,KRAS,STAT3,HHEX,TK1,XPA	10
Antigen Presentation	72h	8.43E-04-1.87E-02	PTPRC,CTSD,ITGB2,LGALS3,CST3,ANXA5,ADA,NAGLU,STAT3	9
Metabolic Disease	72h	1.72E-03-1.72E-02	PTPRC,COL5A1,CTSD,CLN8,CST3,ADA,NAGLU,STAT3,XPA	9
Lipid Metabolism	72h	6.68E-04-1.9E-02	HSPA8,CTSD,ACAT2,INSIG1,ANXA5,NAGLU,LSS,STAT3	8
Cardiovascular System Development	72h	1.43E-03-1.71E-02	COL5A1,ITGB2,LGALS3,CST3,ANXA5,ADA,ACTG2,EGFL7	8
Nervous System	72h	5.72E-03-1.71E-02	STXBP1,DYNLT1,FEZ1,GRIA1,NAGLU,STAT3,XPA	7
Connective Tissue	72h	2.06E-03-1.71E-02	PTPRC,CTSD,ITGB2,LGALS3,CST3,KRAS,ACTG2	7
Neurological Disease	72h	1.72E-03-1.71E-02	CTSD,CLN8,CST3,RNF213,ADA,STAT3,UNG	7
Protein Trafficking	72h	1.25E-03-7.58E-03	DYNLT1,PCNA,ARF4,RAN,NUP214,KRAS,STAT3	7
Carbohydrate Metabolism	72h	5.72E-03-1.9E-02	CTSD,UGDH,ANXA5,NAGLU,STAT3,MVP	6

Gene Expression	72h	5.72E-03-1.71E-02	PCNA,STAT3,SSRP1,CDK1,XPA	5
Tumor Morphology	72h	5.72E-03-1.71E-02	LSP1 (includes EG:16985),CAPN2,KRAS,STAT3,CDK1	5
Cellular Response to	72h	5.72E-03-7.53E-03	PCNA,FEN1,XPA,UNG	4
Organismal Functions	72h	2.17E-03-5.72E-03	ITGB2,GRIA1,NAGLU,TK1	4
Vitamin and Mineral	72h	1.25E-03-1.25E-03	HSPA8,ACAT2,INSIG1,LSS	4
Protein Folding	72h	7.54E-03-7.54E-03	HSPA8,CCT4,BAG2	3
Hair and Skin Development	72h	3.21E-04-1.14E-02	TP53INP1,STAT3,AKAP9	3
RNA Trafficking	72h	2.93E-03-1.8E-02	RAN,NUP214,HHEX	3
Skeletal and Muscular	72h	1.04E-02-1.14E-02	PTPRC,ITGB2,LGALS3	3
Auditory and Vestibular	72h	6.95E-03-1.71E-02	INSIG1,NAGLU	2
Drug Metabolism	72h	5.72E-03-1.14E-02	MVP,UNG	2
Hypersensitivity Response	72h	2.06E-03-1.11E-02	ITGB2,LGALS3	2
Humoral Immune	72h	1.14E-02-1.71E-02	PTPRC,ITGB2	2
Endocrine System	72h	5.72E-03-5.72E-03	HHEX	1
Ophthalmic Disease	72h	5.72E-03-5.72E-03	CST3	1
Energy Production	72h	5.72E-03-5.72E-03	UGDH	1
Respiratory System	72h	1.14E-02-1.14E-02	ADA	1

Ingenuity Pathway analysis
Canonical pathway analysis (48 h)

Ingenuity Canonical Pathways	Time	-log(p-value)	Ratio	Transcripts	Transcripts
CD28 Signaling in T Helper Cells	48h	1.7	0.0152	VAV1,CARD11	2
PKCθ Signaling in T Lymphocytes	48h	1.71	0.0141	VAV1,CARD11	2
T Cell Receptor Signaling	48h	1.84	0.0183	VAV1,CARD11	2
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	48h	2.03	0.0225	VAV1,CARD11	2
Protein Kinase A Signaling	48h	0.35	0.00299	GRK7	1
Actin Cytoskeleton Signaling	48h	0.481	0.00415	VAV1	1
LPS/IL-1 Mediated Inhibition of RXR Function	48h	0.485	0.00424	ALAS1	1
Leukocyte Extravasation Signaling	48h	0.523	0.00503	VAV1	1
Clathrin-mediated Endocytosis Signaling	48h	0.54	0.00513	APOA1	1
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	48h	0.542	0.00476	APOA1	1
Endothelin-1 Signaling	48h	0.552	0.00541	PTGS1	1
Dendritic Cell Maturation	48h	0.556	0.00483	COL2A1 (includes EG:1280)	1
CREB Signaling in Neurons	48h	0.556	0.00498	GRIK2	1
PPARα/RXRα Activation	48h	0.564	0.00535	APOA1	1
Acute Phase Response Signaling	48h	0.58	0.00565	APOA1	1
Arachidonic Acid Metabolism	48h	0.582	0.00485	PTGS1	1
NF-κB Signaling	48h	0.582	0.00571	CARD11	1
Cdc42 Signaling	48h	0.591	0.00562	VAV1	1
B Cell Receptor Signaling	48h	0.625	0.00641	VAV1	1
IL-12 Signaling and Production in Macrophages	48h	0.657	0.00645	APOA1	1
PI3K Signaling in B Lymphocytes	48h	0.66	0.00699	VAV1	1
Ovarian Cancer Signaling	48h	0.665	0.00704	PTGS1	1
LXR/RXR Activation	48h	0.689	0.00735	APOA1	1
Gα12/13 Signaling	48h	0.712	0.00787	VAV1	1
Glycine, Serine and Threonine Metabolism	48h	0.721	0.00676	ALAS1	1
iCOS-iCOSL Signaling in T Helper Cells	48h	0.739	0.0082	VAV1	1
Amyotrophic Lateral Sclerosis Signaling	48h	0.742	0.00833	GRIK2	1
Fc Epsilon RI Signaling	48h	0.746	0.00901	VAV1	1
Natural Killer Cell Signaling	48h	0.753	0.00917	VAV1	1
Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes	48h	0.788	0.0098	VAV1	1
FXR/RXR Activation	48h	0.796	0.0099	APOA1	1
Eicosanoid Signaling	48h	0.885	0.0127	PTGS1	1
Caveolar-mediated Endocytosis Signaling	48h	0.89	0.0118	FLOT2	1
Ephrin B Signaling	48h	0.896	0.0125	VAV1	1

PXR/RXR Activation	48h	0.912	0.0114	ALAS1	1
Glutamate Receptor Signaling	48h	0.96	0.0145	GRIK2	1
Biosynthesis of Steroids	48h	0.98	0.008	FDPS	1
Pentose Phosphate Pathway	48h	1.02	0.0125	DERA	1
Ephrin A Signaling	48h	1.06	0.0192	VAV1	1
Intrinsic Prothrombin Activation Pathway	48h	1.29	0.0312	COL2A1 (includes EG:1280)	1
Role of Lipids/Lipid Rafts in the Pathogenesis of Influenza	48h	1.34	0.0357	FDPS	1

Ingenuity Pathway analysis
Canonical pathway analysis (72 h)

Ingenuity Canonical Pathways	Time	-log(p-value)	Ratio	Transcripts	Transcripts
Purine Metabolism	72h	1.84	0.0149	IMPDH2,ATP1B1,RNF213,RRM2,ADA,RRM1	6
Integrin Signaling	72h	3.01	0.0286	ITGB2,ARF4,ZYX,KRAS,CAPN2,ACTG2	6
Glucocorticoid Receptor Signaling	72h	1.73	0.017	HSPA8,CD247,KRAS,STAT3,CD3D	5
Pyrimidine Metabolism	72h	2.37	0.0233	RRM2,DTYMK,UNG,TK1,RRM1	5
Protein Ubiquitination Pathway	72h	1.21	0.0149	HSPA8,PSMA3,PSMA5,PSMD3	4
PKCθ Signaling in T Lymphocytes	72h	2.31	0.0282	CD247,KRAS,CD3D,MAP3K3	4
T Cell Receptor Signaling	72h	2.55	0.0367	PTPRC,CD247,KRAS,CD3D	4
Primary Immunodeficiency Signaling	72h	3.62	0.0635	PTPRC,ADA,CD3D,UNG	4
G-Protein Coupled Receptor Signaling	72h	0.243	0.0057	P2RY10,KRAS,STAT3	3
Xenobiotic Metabolism Signaling	72h	0.653	0.0102	KRAS,Sult1d1,MAP3K3	3
Phospholipase C Signaling	72h	0.803	0.0115	CD247,KRAS,CD3D	3
Huntington's Disease Signaling	72h	0.871	0.0127	HSPA8,CTSD,CAPN2	3
Actin Cytoskeleton Signaling	72h	0.879	0.0124	KRAS,LIMK2,ACTG2	3
Breast Cancer Regulation by Stathmin1	72h	0.98	0.0144	KRAS,LIMK2,CDK1	3
EIF2 Signaling	72h	1.03	0.0149	KRAS,EIF2S1,RPL10A	3
Clathrin-mediated Endocytosis Signaling	72h	1.04	0.0154	HSPA8,ITGB2,ACTG2	3
IL-8 Signaling	72h	1.04	0.0148	ITGB2,KRAS,LIMK2	3
Sertoli Cell-Sertoli Cell Junction Signaling	72h	1.04	0.0152	KRAS,ACTG2,MAP3K3	3
NRF2-mediated Oxidative Stress Response	72h	1.08	0.0157	CCT7,KRAS,ACTG2	3
Role of NFAT in Regulation of the Immune Response	72h	1.09	0.0152	CD247,KRAS,CD3D	3
Ephrin Receptor Signaling	72h	1.1	0.0151	KRAS,LIMK2,STAT3	3
Cdc42 Signaling	72h	1.17	0.0169	CD247,LIMK2,CD3D	3
B Cell Receptor Signaling	72h	1.27	0.0192	PTPRC,KRAS,MAP3K3	3
CD28 Signaling in T Helper Cells	72h	1.49	0.0227	PTPRC,CD247,CD3D	3
iCOS-iCOSL Signaling in T Helper Cells	72h	1.59	0.0246	PTPRC,CD247,CD3D	3
Type I Diabetes Mellitus Signaling	72h	1.6	0.0248	CD247,IFNGR2,CD3D	3
HGF Signaling	72h	1.68	0.0286	KRAS,STAT3,MAP3K3	3
Paxillin Signaling	72h	1.69	0.0268	ITGB2,KRAS,ACTG2	3
Virus Entry via Endocytic Pathways	72h	1.75	0.03	ITGB2,KRAS,ACTG2	3

VEGF Signaling	72h	1.79	0.0303	KRAS,ACTG2,EIF2S1	3
FAK Signaling	72h	1.83	0.0294	KRAS,CAPN2,ACTG2	3
Apoptosis Signaling	72h	1.84	0.0312	KRAS,CAPN2,CDK1	3
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	72h	1.95	0.0337	CD247,KRAS,CD3D	3
Agrin Interactions at Neuromuscular Junction	72h	2.14	0.0435	ITGB2,KRAS,ACTG2	3
Calcium-induced T Lymphocyte Apoptosis	72h	2.19	0.0429	CD247,CAPN2,CD3D	3
Nur77 Signaling in T Lymphocytes	72h	2.39	0.0476	CD247,CD3D,MAP3K3	3
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	72h	0.275	0.00599	KRAS,STAT3	2
Colorectal Cancer Metastasis Signaling	72h	0.391	0.00778	KRAS,STAT3	2
Signaling by Rho Family GTPases	72h	0.416	0.00791	LIMK2,ACTG2	2
Cardiac Hypertrophy Signaling	72h	0.418	0.0082	KRAS,MAP3K3	2
cAMP-mediated signaling	72h	0.452	0.00913	STAT3,AKAP9	2
Leukocyte Extravasation Signaling	72h	0.51	0.0101	ITGB2,ACTG2	2
ERK/MAPK Signaling	72h	0.534	0.0098	KRAS,STAT3	2
ILK Signaling	72h	0.537	0.0104	ITGB2,ACTG2	2
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	72h	0.54	0.00952	IFNGR2,MAP3K3	2
RhoGDI Signaling	72h	0.56	0.0101	LIMK2,ACTG2	2
CREB Signaling in Neurons	72h	0.563	0.00995	GRIA1,KRAS	2
Gap Junction Signaling	72h	0.581	0.011	KRAS,ACTG2	2
Inositol Phosphate Metabolism	72h	0.584	0.0101	LIMK2,CDK1	2
Acute Phase Response Signaling	72h	0.602	0.0113	KRAS,STAT3	2
NF-κB Signaling	72h	0.606	0.0114	KRAS,MAP3K3	2
Aldosterone Signaling in Epithelial Cells	72h	0.606	0.0116	HSPA8,KRAS	2
Regulation of eIF4 and p70S6K Signaling	72h	0.669	0.0115	KRAS,EIF2S1	2
Synaptic Long Term Depression	72h	0.733	0.0135	GRIA1,KRAS	2
PI3K Signaling in B Lymphocytes	72h	0.738	0.014	PTPRC,KRAS	2
GNRH Signaling	72h	0.768	0.0137	KRAS,MAP3K3	2
Nicotinate and Nicotinamide Metabolism	72h	0.817	0.0145	LIMK2,CDK1	2
CCR3 Signaling in Eosinophils	72h	0.828	0.0159	KRAS,LIMK2	2
Renin-Angiotensin Signaling	72h	0.834	0.0159	KRAS,STAT3	2
Hereditary Breast Cancer Signaling	72h	0.84	0.0157	KRAS,CDK1	2
IL-6 Signaling	72h	0.846	0.0161	KRAS,STAT3	2
RhoA Signaling	72h	0.864	0.0175	LIMK2,ACTG2	2

Synaptic Long Term Potentiation	72h	0.87	0.0175	GRIA1,KRAS	2
Role of Tissue Factor in Cancer	72h	0.877	0.0175	KRAS,LIMK2	2
Amyotrophic Lateral Sclerosis Signaling	72h	0.883	0.0167	GRIA1,CAPN2	2
NGF Signaling	72h	0.883	0.0172	KRAS,MAP3K3	2
Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency	72h	0.889	0.0175	KRAS,STAT3	2
Pancreatic Adenocarcinoma Signaling	72h	0.896	0.0168	KRAS,STAT3	2
Natural Killer Cell Signaling	72h	0.902	0.0183	CD247,KRAS	2
Rac Signaling	72h	0.909	0.0164	KRAS,LIMK2	2
IGF-1 Signaling	72h	0.951	0.0189	KRAS,STAT3	2
Mouse Embryonic Stem Cell Pluripotency	72h	0.988	0.0202	KRAS,STAT3	2
SAPK/JNK Signaling	72h	0.988	0.0196	KRAS,MAP3K3	2
HMGB1 Signaling	72h	0.995	0.02	IFNGR2,KRAS	2
p53 Signaling	72h	1	0.0208	PCNA,TP53INP1	2
CTLA4 Signaling in Cytotoxic T Lymphocytes	72h	1.01	0.0204	CD247,CD3D	2
PAK Signaling	72h	1.02	0.0187	KRAS,LIMK2	2
Pyruvate Metabolism	72h	1.03	0.0144	ACAT2,HAGHL	2
OX40 Signaling Pathway	72h	1.07	0.0213	CD247,CD3D	2
Ceramide Signaling	72h	1.09	0.0227	CTSD,KRAS	2
Lysine Degradation	72h	1.1	0.0146	ACAT2,DLST	2
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	72h	1.11	0.0235	CD247,CD3D	2
Acute Myeloid Leukemia Signaling	72h	1.14	0.0244	KRAS,STAT3	2
PDGF Signaling	72h	1.14	0.0253	KRAS,STAT3	2
Caveolar-mediated Endocytosis Signaling	72h	1.15	0.0235	ITGB2,ACTG2	2
Prolactin Signaling	72h	1.15	0.025	KRAS,STAT3	2
HER-2 Signaling in Breast Cancer	72h	1.15	0.025	ITGB2,KRAS	2
NF-κB Activation by Viruses	72h	1.17	0.0244	ITGB2,KRAS	2
CCR5 Signaling in Macrophages	72h	1.17	0.0213	CD247,CD3D	2
Chemokine Signaling	72h	1.18	0.0274	KRAS,LIMK2	2
FLT3 Signaling in Hematopoietic Progenitor Cells	72h	1.19	0.027	KRAS,STAT3	2
IL-3 Signaling	72h	1.2	0.027	KRAS,STAT3	2
T Helper Cell Differentiation	72h	1.22	0.0278	IFNGR2,STAT3	2
Macropinocytosis Signaling	72h	1.24	0.0263	ITGB2,KRAS	2
JAK/Stat Signaling	72h	1.25	0.0286	KRAS,STAT3	2
ERK5 Signaling	72h	1.3	0.0312	KRAS,MAP3K3	2
GM-CSF Signaling	72h	1.3	0.0299	KRAS,STAT3	2
Role of JAK1 and JAK3 in γc Cytokine Signaling	72h	1.31	0.0299	KRAS,STAT3	2

IL-15 Signaling	72h	1.32	0.0299	KRAS,STAT3	2
Thrombopoietin Signaling	72h	1.35	0.0317	KRAS,STAT3	2
ErbB2-ErbB3 Signaling	72h	1.39	0.0339	KRAS,STAT3	2
Role of CHK Proteins in Cell Cycle Checkpoint Control	72h	1.42	0.0357	PCNA,CDK1	2
CNTF Signaling	72h	1.45	0.0364	KRAS,STAT3	2
Hematopoiesis from Pluripotent Stem Cells	72h	1.45	0.0312	CD247,CD3D	2
MSP-RON Signaling Pathway	72h	1.53	0.0392	ITGB2,ACTG2	2
Oncostatin M Signaling	72h	1.79	0.0571	KRAS,STAT3	2
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	72h	2.08	0.0741	IFNGR2,STAT3	2
GADD45 Signaling	72h	2.28	0.0909	PCNA,CDK1	2
Mismatch Repair in Eukaryotes	72h	2.33	0.0833	PCNA,FEN1	2
Fatty Acid Metabolism	72h	0.21	0.00546	ACAT2	1
CXCR4 Signaling	72h	0.22	0.00595	KRAS	1
Tight Junction Signaling	72h	0.228	0.00613	ACTG2	1
Glioblastoma Multiforme Signaling	72h	0.228	0.00595	KRAS	1
Cellular Effects of Sildenafil (Viagra)	72h	0.241	0.00645	ACTG2	1
eNOS Signaling	72h	0.251	0.00662	HSPA8	1
Aryl Hydrocarbon Receptor Signaling	72h	0.253	0.00629	CTSD	1
Hepatic Fibrosis / Hepatic Stellate Cell Activation	72h	0.257	0.0068	IFNGR2	1
Cardiac β-adrenergic Signaling	72h	0.257	0.00649	AKAP9	1
Ovarian Cancer Signaling	72h	0.269	0.00704	KRAS	1
Insulin Receptor Signaling	72h	0.274	0.00735	KRAS	1
P2Y Purigenic Receptor Signaling Pathway	72h	0.276	0.00714	KRAS	1
p70S6K Signaling	72h	0.28	0.00752	KRAS	1
Estrogen Receptor Signaling	72h	0.285	0.00735	KRAS	1
Arginine and Proline Metabolism	72h	0.287	0.00565	RARS	1
PI3K/AKT Signaling	72h	0.294	0.00719	KRAS	1
14-3-3-mediated Signaling	72h	0.302	0.0082	KRAS	1
Atherosclerosis Signaling	72h	0.304	0.00763	ITGB2	1
Gα12/13 Signaling	72h	0.304	0.00787	KRAS	1
fMLP Signaling in Neutrophils	72h	0.315	0.00781	KRAS	1
PTEN Signaling	72h	0.318	0.00781	KRAS	1
Glycolysis/Gluconeogenesis	72h	0.323	0.00769	PGAM1	1
Fc Epsilon RI Signaling	72h	0.331	0.00901	KRAS	1
Neuropathic Pain Signaling In Dorsal Horn Neurons	72h	0.334	0.00893	GRIA1	1
Cholecystokinin/Gastrin-mediated Signaling	72h	0.34	0.00943	KRAS	1
HIF1α Signaling	72h	0.346	0.00935	KRAS	1
Glioma Signaling	72h	0.359	0.00893	KRAS	1
Telomerase Signaling	72h	0.362	0.0098	KRAS	1

Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes	72h	0.365	0.0098	ACTG2	1
G Beta Gamma Signaling	72h	0.365	0.00862	KRAS	1
α-Adrenergic Signaling	72h	0.369	0.00952	KRAS	1
Valine, Leucine and Isoleucine Degradation	72h	0.369	0.00935	ACAT2	1
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	72h	0.372	0.00943	EIF2S1	1
PPAR Signaling	72h	0.375	0.00943	KRAS	1
Starch and Sucrose Metabolism	72h	0.379	0.00602	UGDH	1
Neuregulin Signaling	72h	0.382	0.0098	KRAS	1
Chronic Myeloid Leukemia Signaling	72h	0.382	0.00962	KRAS	1
CDK5 Signaling	72h	0.39	0.0106	KRAS	1
Crosstalk between Dendritic Cells and Natural Killer Cells	72h	0.393	0.0105	ACTG2	1
Bladder Cancer Signaling	72h	0.401	0.011	KRAS	1
RANK Signaling in Osteoclasts	72h	0.401	0.0105	MAP3K3	1
FGF Signaling	72h	0.401	0.0111	STAT3	1
Melanocyte Development and Pigmentation Signaling	72h	0.405	0.0109	KRAS	1
Regulation of Actin-based Motility by Rho	72h	0.409	0.011	ACTG2	1
Prostate Cancer Signaling	72h	0.412	0.0103	KRAS	1
ErbB Signaling	72h	0.412	0.0115	KRAS	1
Butanoate Metabolism	72h	0.416	0.00781	ACAT2	1
Leptin Signaling in Obesity	72h	0.421	0.0114	STAT3	1
TGF-β Signaling	72h	0.421	0.0112	KRAS	1
Propanoate Metabolism	72h	0.421	0.00826	ACAT2	1
VEGF Family Ligand-Receptor Interactions	72h	0.425	0.0119	KRAS	1
Reelin Signaling in Neurons	72h	0.437	0.0122	ITGB2	1
Cyclins and Cell Cycle Regulation	72h	0.442	0.0114	CDK1	1
Aminoacyl-tRNA Biosynthesis	72h	0.455	0.0132	RARS	1
Cysteine Metabolism	72h	0.46	0.0111	Sult1d1	1
LPS-stimulated MAPK Signaling	72h	0.465	0.0122	KRAS	1
BMP signaling pathway	72h	0.465	0.0125	KRAS	1
IL-10 Signaling	72h	0.47	0.0128	STAT3	1
IL-17 Signaling	72h	0.47	0.0135	KRAS	1
Growth Hormone Signaling	72h	0.47	0.0133	STAT3	1
Renal Cell Carcinoma Signaling	72h	0.47	0.0135	KRAS	1
Non-Small Cell Lung Cancer Signaling	72h	0.475	0.0127	KRAS	1
GDNF Family Ligand-Receptor Interactions	72h	0.475	0.0137	KRAS	1
Erythropoietin Signaling	72h	0.48	0.0128	KRAS	1

IL-4 Signaling	72h	0.48	0.0137	KRAS	1
Neurotrophin/TRK Signaling	72h	0.48	0.0137	KRAS	1
Pentose and Glucuronate Interconversions	72h	0.49	0.00704	UGDH	1
Chondroitin Sulfate Biosynthesis	72h	0.495	0.0147	Sult1d1	1
Angiopoietin Signaling	72h	0.495	0.0135	KRAS	1
Antiproliferative Role of Somatostatin Receptor 2	72h	0.495	0.0141	KRAS	1
Role of MAPK Signaling in the Pathogenesis of Influenza	72h	0.495	0.0147	KRAS	1
Mitotic Roles of Polo-Like Kinase	72h	0.501	0.0145	CDK1	1
Retinoic acid Mediated Apoptosis Signaling	72h	0.501	0.0147	DAP3	1
N-Glycan Biosynthesis	72h	0.501	0.0123	MAN1B1	1
IL-17A Signaling in Airway Cells	72h	0.506	0.0139	STAT3	1
Glutamate Receptor Signaling	72h	0.512	0.0145	GRIA1	1
Estrogen-Dependent Breast Cancer Signaling	72h	0.512	0.0143	KRAS	1
CD40 Signaling	72h	0.517	0.0143	STAT3	1
Nitrogen Metabolism	72h	0.523	0.0084	37316	1
Biosynthesis of Steroids	72h	0.529	0.008	LSS	1
ErbB4 Signaling	72h	0.529	0.0152	KRAS	1
TREM1 Signaling	72h	0.535	0.0141	STAT3	1
Myc Mediated Apoptosis Signaling	72h	0.541	0.0164	KRAS	1
Glioma Invasiveness Signaling	72h	0.547	0.0167	KRAS	1
Keratan Sulfate Biosynthesis	72h	0.554	0.0175	Sult1d1	1
ATM Signaling	72h	0.554	0.0169	CDK1	1
Actin Nucleation by ARP-WASP Complex	72h	0.56	0.0152	KRAS	1
IL-2 Signaling	72h	0.567	0.0172	KRAS	1
Glycosaminoglycan Degradation	72h	0.574	0.0172	NAGLU	1
Endometrial Cancer Signaling	72h	0.574	0.0175	KRAS	1
Semaphorin Signaling in Neurons	72h	0.588	0.0192	LIMK2	1
nNOS Signaling in Neurons	72h	0.588	0.0192	CAPN2	1
Amyloid Processing	72h	0.588	0.0179	CAPN2	1
CD27 Signaling in Lymphocytes	72h	0.595	0.0175	MAP3K3	1
EGF Signaling	72h	0.602	0.0192	STAT3	1
Citrate Cycle	72h	0.602	0.0175	DLST	1
iNOS Signaling	72h	0.626	0.0189	IFNGR2	1
FcγRIIB Signaling in B Lymphocytes	72h	0.642	0.0169	KRAS	1
Melanoma Signaling	72h	0.651	0.0217	KRAS	1
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	72h	0.651	0.0204	CDK1	1
Thyroid Cancer Signaling	72h	0.678	0.0238	KRAS	1

Role of PKR in Interferon Induction and Antiviral Response	72h	0.687	0.0217	EIF2S1	1
Mechanisms of Viral Exit from Host Cells	72h	0.687	0.0222	ACTG2	1
Transcriptional Regulatory Network in Embryonic Stem Cells	72h	0.687	0.025	STAT3	1
Sulfur Metabolism	72h	0.728	0.0172	Sult1d1	1
Nucleotide Excision Repair Pathway	72h	0.74	0.0286	XPA	1
IL-9 Signaling	72h	0.751	0.025	STAT3	1
Role of JAK2 in Hormone-like Cytokine Signaling	72h	0.751	0.0278	STAT3	1
Interferon Signaling	72h	0.751	0.0278	IFNGR2	1
B Cell Development	72h	0.775	0.0303	PTPRC	1
Sonic Hedgehog Signaling	72h	0.8	0.0303	CDK1	1
N-Glycan Degradation	72h	0.843	0.037	MAN1B1	1
Cell Cycle Control of Chromosomal Replication	72h	0.843	0.0323	MCM5	1
Role of JAK family kinases in IL-6-type Cytokine Signaling	72h	0.874	0.037	STAT3	1
IL-22 Signaling	72h	0.89	0.04	STAT3	1
Estrogen-mediated S-phase Entry	72h	0.89	0.0357	CDK1	1
Polyamine Regulation in Colon Cancer	72h	0.907	0.0345	KRAS	1
Nucleotide Sugars Metabolism	72h	0.965	0.0154	UGDH	1
RAN Signaling	72h	0.986	0.0417	RAN	1
Endoplasmic Reticulum Stress Pathway	72h	1.01	0.0556	EIF2S1	1
Synthesis and Degradation of Ketone Bodies	72h	1.03	0.0526	ACAT2	1